

SQ	Sequence 15 AA;		Best Local Similarity 92.9%; Pred. No. 1.4e-06;	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
	Query Match 98.8%; Score 81; DB 3; Length 15;		Qy 1 CAWYASRGIRPVGR 14		
	Best Local Similarity 100.0%; Pred. No. 2.8e-07;		Db 1 CAWYASRGIRPVGR 14		
	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 CAWYASRGIRPVGR 14				
DB	1 CAWYASRGIRPVGR 14				
RESULT 2					
ID	AAW1400	Standard; peptide; 15 AA.			
XX	AAW1400				
AC	AAW1400;				
XX					
DT	06-APR-1998	(first entry)			
XX					
DE	Synthetic ligand 19P2-L31 peptide II.				
XX					
G	Protein-coupled receptor; ligand binding; pharmaceutical; modulator;				
XX					
KW	pituitary; central nervous system; pancreas; prophylactic;				
KW	therapeutic agent; antigen.				
XX					
OS	Synthetic.				
PN	WO924436-A2.				
XX					
PD	10-JUL-1997.				
XX					
PF	26-DEC-1996; 96WO-JP003821.				
XX					
PR	28-DEC-1995; 95JP-0034371.				
PR	15-MAR-1996; 96JP-00059419.				
PR	12-AUG-1996; 96JP-00211905.				
PR	18-SEP-1996; 96JP-00246573.				
XX					
(TAKE)	TAKEDA CHEM IND LTD.				
XX					
PI	Hinuma S, Habata Y, Kawahata Y, Hosoya M, Fujii R, Fukusumi S;				
PI	Kitada C,				
XX					
DR	1997-363672/33.				
XX					
PT	Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland.				
XX					
PS	Example 43; Page 151; 258PP; English.				
XX					
This peptide contains the partial C-terminal sequence of the synthetic ligand polypeptide 19P2-L31 which is capable of binding to a G protein-coupled receptor protein. This peptide is used as an antigen to prepare rabbit anti-bovine 19P2-L31 antibodies which are used in binding assays. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hypokinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyperphagia, hyperlipididaemia, hypercholesterolemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, rheumatoid arthritis, asthma, rhinitis, spinal injury, transient brain ischaemia, epilepsy, amyotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein					
XX	Sequence 15 AA;				
Query Match 93.9%; Score 77; DB 2; Length 15;					
Query Match	93.9%; Score 77; DB 2; Length 15;				
Best Local Similarity 92.9%; Pred. No. 1.4e-06;					
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					

XX Matsumoto H, Kitada C, Hinuma S;
 PI WPI: 2000-452228/39.
 DR XX
 Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
 PT XX
 Disclosure; Page 63; 72pp; Japanese.
 XX This invention describes novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion promoter.
 XX SQ Sequence 20 AA;
 Query Match 87.8%; Score 72; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PT XX
 RESULT 9
 AAB9092 ID AAB9092 standard; peptide; 20 AA.
 XX AC AAB9092;
 XX DT 22-JUN-2001 (first entry)
 XX DB Prolactin releasing peptide SEQ ID NO:166.
 XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX OS Homo sapiens.
 XX CS Synthetic.
 XX EN WO200069900-A2.
 XX DD 23-NOV-2000.
 XX PF 17-MAY-2000; 2000WO-US013576.
 XX PR 17-MAY-1999; 99US-0134406P.
 XX PR 10-SEP-1999; 99US-0153416P.
 XX PR 15-OCT-1999; 99US-0159703P.
 XX PA (CONJ-) CONJUCHEM INC.
 XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX DR WPI: 2001-11205/12.
 XX Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
 XX Disclosure; Page 244; 733pp; English.
 XX The present invention describes a modified therapeutic peptide (I) and a comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxy/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, Growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intercellular uptake and interference with physiological processes.
 CC AA90829 to AAB9241 represent peptides which can be used in the exemplification of the present invention

CC Sequence 20 AA;
 Query Match 87.8%; Score 72; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AWYASRGIRPYGR 14
 DB 7 AWYASRGIRPYGR 19

RESULT 10
 ARG62534 ID AAG62534 standard; peptide; 20 AA.
 XX AC AAG62534;
 XX DT 24-AUG-2001 (first entry)
 XX Human CRH releasing protein related peptide SEQ ID NO: 35.
 XX DE Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
 KW Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
 KW analgesic; hyperadrenocorticism; hypoadrenocorticism;
 KW Addison's disease; adrenal gland hyperfunction; obesity.
 XX Homo sapiens
 XX OS Homo sapiens
 XX PN WO200135984-A1.
 XX PD 25-MAY-2001.
 XX PA (TAKA) TAKEDA CHEM IND LTD.
 XX PI Kitada C, Matsumoto H, Hinuma S;
 XX DR WPI: 2001-355552/37.
 XX PT Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion.
 XX PS Claim 4; Page 75; 90pp; Japanese.
 XX CC The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperadrenocorticism, Addison's disease (including bordom, nausea, pigmentation, hypogonadism, hair loss, and hypertension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the invention

XX	SQ Sequence 20 AA;	Query Match Best Local Similarity 100.0%; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DB 4; Length 20; Pred. No. 1.5e-05; DB 5; Length 20; Pred. No. 1.5e-05;	Db 7 AWYASRGIRPVGR 19
QY	2 AWYASRGIRPVGR 14	RESULT 12 ABU60846 standard; peptide; 20 AA.		
Db	7 AWYASRGIRPVGR 19	ID ABU60846; XX AC ABU60846; XX DT 06-MAY-2003 (first entry)		
XX		Peptide production by gene recombination associated peptide #30.		
AAE26404		XX Peptide Production; low-molecular peptide; Kiss-1; GPR8 ligand;		
ID AAE26404	standard; peptide; 20 AA.	XX Gene recombination.		
AC AAE26404;		XX Homo sapiens.		
XX		XX OS WO200292829-A1.		
DT 13-DEC-2002	(first entry)	XX PN DE 21-NOV-2002.		
XX	Human PrRP-31 C-terminal peptide, PrRP-20.	XX PD 16-MAY-2002; 2002WO-JP004735.		
XX	Human; wakefulness; sleep disorder; prolactin releasing peptide receptor; PrRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea; insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure; anticonvulsant.	XX PR 17-MAY-2001; 2001EP-00147341.		
XX	Homo sapiens.	XX PA (TAKEDA) CHEM IND LTD.		
OS US2002037533-A1.		XX PI Nishimura O, Suenaga M, Ito T, Kitada C; DR WPI: 2003-122302/12.		
PN 28-MAR-2002.		XX PT Process for producing peptides e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.		
XX 17-AUG-2001; 2001US-00932161.		XX PT PT		
XX 28-APR-2000; 2000US-00560915.		XX Disclosure; Page 68; 87pp; Japanese.		
XX (CIVB/) CIVELLI O. PA (LINS/) LIN S.		XX CC The invention describes a method of producing a peptide comprising the excision of the N and C-terminal s of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention		
PA (LINS/) LIN S.		XX PS Disclosure; Page 68; 87pp; Japanese.		
PI CIVELLI O, Lin S;		XX CC Sequence 20 AA;		
XX WPI: 2002-403931/43.		Query Match Best Local Similarity 100.0%; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
XX	Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or antagonist.	QY 2 AWYASRGIRPVGR 14		
XX	WPI Disclosure; Page 25; 35pp; English.	Db 7 AWYASRGIRPVGR 19		
PS	The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing Peptide (PrRP) receptor (GPR10) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. PrRP receptor agonists may be used to treat common disorders which lead to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and psychogenic hypersomnia. PrRP receptor antagonists are useful for promoting sleep and for treating insomnia such as adjustment sleep disorder and psychophysiological insomnia. The present sequence is human PrRP-31 C-terminal peptide, PrRP-20	RESULT 13 AAW1395 standard; peptide; 21 AA.		
SQ Sequence 20 AA;		ID AAW1395 DT 06-APR-1998 (first entry)		
XX	Screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing Peptide (PrRP) receptor (GPR10) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. PrRP receptor agonists may be used to treat common disorders which lead to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and psychogenic hypersomnia. PrRP receptor antagonists are useful for promoting sleep and for treating insomnia such as adjustment sleep disorder and psychophysiological insomnia. The present sequence is human PrRP-31 C-terminal peptide, PrRP-20	XX AC AAW1395; XX DT 06-APR-1998 (first entry)		
QY 87.8%; Score 72; DB 5; Length 20; Best Local Similarity 100.0%; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		XX DE Human type G protein-coupled receptor ligand fragment 5.		
XX	Query Match 2 ANYASRGIRPVGR 14	XX KW G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic;		

therapeutic agent.

XX

Homo sapiens.

OS

WO9724436-A2.

PN

XX

10-JUL-1997.

XX

26-DEC-1996;

XX

96WO-JP003821.

PR

28-DEC-1995;

XX

95JP-00343371.

PR

15-MAR-1996;

XX

96JP-00059419.

PR

12-AUG-1996;

XX

96JP-00211805.

PR

18-SEP-1996;

XX

96JP-00246573.

PA

(TAKE) TAKEDA CHEM IND LTD.

XX

WPI; 2000-452298/39.

XX

Homo sapiens.

OS

XX

WO200038704-A1.

PN

XX

06-JUL-2000.

PD

XX

22-DEC-1999;

XX

99WO-JP007199.

PR

25-DEC-1998;

XX

98JP-00369585.

PA

(TAKE) TAKEDA CHEM IND LTD.

XX

Matsumoto H,

Kitada C,

Hiruma S;

XX

WPI; 2000-452298/39.

XX

Physiologically active polypeptide recognized as ligand by G protein-

PT

coupled receptor protein, for promoting secretion of oxytocin, as drugs

PT

for diseases relating to oxytocin secretion and in veterinary medicine.

XX

Disclosure; Page 63; 72pp; Japanese.

XX

Physiologically active polypeptide recognized as ligand by G protein-

PT

coupled receptor protein, for promoting secretion of oxytocin, as drugs

PT

for diseases relating to oxytocin secretion and in veterinary medicine.

XX

Homo sapiens.

OS

XX

WO9724436-A2.

PN

XX

10-JUL-1997.

XX

26-DEC-1996;

XX

96WO-JP003821.

PR

28-DEC-1995;

XX

95JP-00343371.

PR

15-MAR-1996;

XX

96JP-00059419.

PR

12-AUG-1996;

XX

96JP-00211805.

PR

18-SEP-1996;

XX

96JP-00246573.

PA

(TAKE) TAKEDA CHEM IND LTD.

XX

WPI; 2000-452298/39.

XX

Physiologically active polypeptide recognized as ligand by G protein-

PT

coupled receptor protein, for promoting secretion of oxytocin, as drugs

PT

for diseases relating to oxytocin secretion and in veterinary medicine.

XX

Homo sapiens.

OS

XX

WO200038704-A1.

PN

XX

06-JUL-2000.

PD

XX

22-DEC-1999;

XX

99WO-JP007199.

PR

25-DEC-1998;

XX

98JP-00369585.

PA

(TAKE) TAKEDA CHEM IND LTD.

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WPI; 2000-452298/39.

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Physiologically active polypeptide recognized as ligand by G protein-

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coupled receptor protein, for promoting secretion of oxytocin, as drugs

PT

for diseases relating to oxytocin secretion and in veterinary medicine.

XX

Homo sapiens.

OS

XX

WO200038704-A1.

PN

XX

06-JUL-2000.

PD

XX

22-DEC-1999;

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99WO-JP007199.

PR

25-DEC-1998;

XX

98JP-00369585.

PA

(TAKE) TAKEDA CHEM IND LTD.

XX

WPI; 2000-452298/39.

XX

Physiologically active polypeptide recognized as ligand by G protein-

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coupled receptor protein, for promoting secretion of oxytocin, as drugs

PT

for diseases relating to oxytocin secretion and in veterinary medicine.

XX

Homo sapiens.

OS

XX

WO9724436-A2.

PN

XX

10-JUL-1997.

XX

26-DEC-1996;

XX

96WO-JP003821.

PR

28-DEC-1995;

XX

95JP-00343371.

PR

15-MAR-1996;

XX

96JP-00059419.

PR

12-AUG-1996;

XX

96JP-00211805.

PR

18-SEP-1996;

XX

96JP-00246573.

PA

(TAKE) TAKEDA CHEM IND LTD.

XX

WPI; 2000-452298/39.

XX

Physiologically active polypeptide recognized as ligand by G protein-

PT

coupled receptor protein, for promoting secretion of oxytocin, as drugs

PT

for diseases relating to oxytocin secretion and in veterinary medicine.

XX

Homo sapiens.

OS

XX

WO9724436-A2.

PN

XX

10-JUL-1997.

XX

26-DEC-1996;

XX

96WO-JP003821.

PR

28-DEC-1995;

XX

95JP-00343371.

PR

15-MAR-1996;

XX

96JP-00059419.

PR

12-AUG-1996;

XX

96JP-00211805.

PR

18-SEP-1996;

XX

96JP-00246573.

PA

(TAKE) TAKEDA CHEM IND LTD.

XX

WPI; 2000-452298/39.

XX

Physiologically active polypeptide recognized as ligand by G protein-

PT

coupled receptor protein, for promoting secretion of oxytocin, as drugs

PT

for diseases relating to oxytocin secretion and in veterinary medicine.

XX

Homo sapiens.

OS

XX

WO9724436-A2.

PN

XX

10-JUL-1997.

XX

26-DEC-1996;

XX

96WO-JP003821.

PR

28-DEC-1995;

XX

95JP-00343371.

PR

15-MAR-1996;

XX

96JP-00059419.

PR

12-AUG-1996;

XX

96JP-00211805.

PR

18-SEP-1996;

XX

96JP-00246573.

PA

(TAKE) TAKEDA CHEM IND LTD.

XX

WPI; 2000-452298/39.

XX

Physiologically active polypeptide recognized as ligand by G protein-

PT

coupled receptor protein, for promoting secretion of oxytocin, as drugs

PT

for diseases relating to oxytocin secretion and in veterinary medicine.

XX

Homo sapiens.

OS

XX

WO9724436-A2.

PN

XX

10-JUL-1997.

XX

26-DEC-1996;

XX

96WO-JP003821.

PR

28-DEC-1995;

XX

95JP-00343371.

PR

15-MAR-1996;

XX

96JP-00059419.

PR

12-AUG-1996;

XX

96JP-00211805.

PR

18-SEP-1996;

XX

96JP-00246573.

PA

(TAKE) TAKEDA CHEM IND LTD.

XX

WPI; 2000-452298/39.

XX

Physiologically active polypeptide recognized as ligand by G protein-

PF 16-MAY-2002; 2002WO-JP004735.
 PS Disclosure; Page 27; 73pp; Japanese.
 XX
 PR 17-MAY-2001; 2001JP-00147341.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PT Nishimura O, Suenaga M, Ito T, Kitada C;
 XX
 DR WPI; 2003-129302/12.
 PT Processes for producing peptides e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
 PT
 PT Disclosure; Page 69; 87pp; Japanese.
 XX
 PS The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
 XX
 Sequence 22 AA;
 Query Match 87.8%; Score 72; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19
 RESULT 21
 ID AAY49299 standard; peptide; 30 AA.
 XX
 AC AAY49299;
 DT 22-FEB-2000 (first entry)
 XX
 DE 19P2 ligand peptide fragment.
 XX
 KW Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
 KW pituitary; regulatory mechanism; central nervous system; pancreatic.
 XX
 OS Homo sapiens.
 XX
 FH Key-Modified-site Location/Qualifiers
 FT 30 /note= "C-terminal amide"
 XX
 PN WO9860112-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-JP002650.
 XX
 PR 21-MAY-1998; 98JP-00140293.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Matsushita H, Kitada C, Hinuma S;
 XX
 DR WPI; 2000-039381/03.
 PT New monoclonal antibodies, useful in diagnosis, as drugs and in studying diseases related to ligand abnormality.
 PT

XX Disclosure; Page 27; 73pp; Japanese.
 PS The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand SQ Sequence 30 AA;
 XX
 Query Match 87.8%; Score 72; DB 3; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30
 RESULT 22
 ID AAW31391 standard; peptide; 31 AA.
 XX
 AC AAW31391;
 XX
 DT 06-APR-1998 (First entry)
 XX Human type G protein-coupled receptor ligand fragment 1.
 DE XX
 KW G protein-coupled receptor; ligand binding; pharmaceutical; modulator;
 KW pituitary; central nervous system; pancreas; prophylactic;
 KW therapeutic agent.
 OS XX
 PN WO9724436-A2.
 XX
 PD 10-JUL-1997.
 XX
 PP 26-DEC-1996; 96WO-JP003821.
 XX
 PR 28-DEC-1995; 95JP-00343371.
 PR 15-MAR-1996; 96JP-00059419.
 PR 12-AUG-1996; 96JP-00211805.
 PR 18-SEP-1996; 96JP-00246573.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Hinuma S, Habata Y, Kawamata Y, Hosoya M, Fujii R, Fukushima S;
 PI Kitada C;
 XX
 DR WPI; 1997-363672/33.
 DR N-PSDB; AAV02428.
 XX
 PT Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland.
 XX
 PS Claim 2; Page 184; 258pp; English.
 XX
 CC This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 23 to 53 of the sequence represented in AAW11390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hypoglycemic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, or disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
 CC

CC growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceraidaemia, hyperprolactinaemia, hypertension, Turner's syndrome, neurosis, asthma, cancer, pancreatitis, renal disease, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amyotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assay can also be developed to screen compounds which are capable of altering the binding activity of the G protein-coupled receptor protein

XX ligand affecting activation of the G protein-coupled receptor protein

Sequence 31 AA;

Query Match 87.8%; Score 72; DB 2; Length 31;

Best Local Similarity 100.0%; Pred. No. 2.4e-05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPYGR 14

Db 18 AWYASRGIRPYGR 30

RESULT 23

AAW87615 standard; peptide; 31 AA.

ID AAW87615.

XX

AC AAW87615;

XX

DT 29-MAR-1999 (first entry)

XX

DE Human 19P2 ligand.

XX

KW 19P2 ligand; G protein coupled receptor; pituitary;

XX prolactin releasing peptide; human; dementia; breast cancer; therapy.

XX

OS Homo sapiens.

XX

EP887417-A2.

XX

PD 30-DEC-1998.

XX

PP 25-JUN-1998;

XX

PR 98EP-00111725.

XX

PR 27-JUN-1997;

XX

(TAKE) TAKEDA CHEM IND LTD.

XX

PI Suenaga M, Moriya T, Tanaka Y, Nishimura O;

XX

DR WPI; 1999-047884/05.

XX

PT Producing a 19P2 pituitary G protein receptor ligand - by cleavage of a fusion protein, useful for preventing and treating dementia, breast cancer, renal failure and autoimmune disease.

XX

PS Claim 5; Page 35; 56pp; English.

XX

This is the amino acid sequence of the human pituitary G protein-coupled receptor ligand 19P2L. A method suitable for commercial high-level production of 19P2L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with human basic fibroblast growth factor (see AAV8376-97) that has been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanylation followed by ammonolysis. 19P2L has prolactin secretion-stimulating and (at high doses) prolactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including: senile dementia, cerebrovascular dementia and dementia associated with:

CC genealogical disorders (e.g. Alzheimer's disease, Parkinson's disease, Pick's disease, Huntington's disease, infectious diseases (e.g. Creutzfeldt-Jkob's), endocrine or metabolic disease or toxicosis (e.g. hypothyroidism, vitamin B12 deficiency, alcoholism, intoxication by drugs, metal and organic compounds) tumourigenic diseases (e.g. brain tumour), traumatic diseases (e.g. chronic subarachnoidal hemorrhage, and other types of dementia, depression, hyperactive child syndrome

CC (microencephalopathy) and disturbance of consciousness. It is also useful CC for prevention and treatment of diseases associated with prolactin hypo- CC and hypersecretion respectively, including: hyperprolactinaemia, CC pituitary adenoma, breast cancer, infertility, impotence and autoimmune CC disease (hyposecretion disorders), and seminal vesicle hypoplasia, CC osteoporosis, menopausal syndrome and renal failure (hyposecretion CC disorders). The 19P2 polypeptide/amide is also useful as a test reagent CC for study of the prolactin secretory function or as a lactagogue in CC mammalian farm animals

XX Sequence 31 AA;

Query Match 87.8%; Score 72; DB 2; Length 31;

Best Local Similarity 100.0%; Pred. No. 2.4e-05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPYGR 14

Db 18 AWYASRGIRPYGR 30

RESULT 24

AAW97235 standard; peptide; 31 AA.

ID AAW97235

XX

AC AAW97235;

XX

DT 06-MAY-1999 (first entry)

XX

DE Human type ligand polypeptide fragment.

XX

KW Rat type ligand; modulation; prolactin secretion;

XX G protein-coupled receptor; GPCR; hyboovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmenopathy; autoimmune disease; prolactinoma; infertility; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castillo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; interruption mole; abortion; unthrifly fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.

XX

OS Homo sapiens.

XX

PN WO958962-A1.

XX

PD 30-DEC-1998.

XX

PP 30-JUN-1998;

XX

PR 98RO-JP002765.

XX

PR 23-JUN-1997;

XX

(TAKE) TAKEDA CHEM IND LTD.

XX

PI Hinuma S, Kawamata Y, Fujii R, Matsumoto H;

XX

DR WPI; 1999-105614/09.

XX

PT Use of G protein-coupled receptor ligands - for modulating prolactin

XX PT secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy.

XX

PA Claim 3; Page 159; 241pp; English.

XX

The present sequence represents a human type ligand fragment. It is used CC in the course of the invention. The specification describes an agent for CC modulating prolactin secretion which comprises a ligand polypeptide or a CC modulator, a G protein-coupled receptor (GPR) protein. The agents for CC promoting prolactin secretion can be used for treating or preventing CC hypogonadism, gonecyst cacogenesis, menopausal syndrome, euthyroid or CC hypometabolism. They can be used for promoting lactation in a domestic CC mammal and as an aphrodisiac. The agents for inhibiting prolactin CC secretion can be used for treating or preventing pituitary adenomatosis,

CC brain tumour, emmeniopathy, autoimmune disease, prolactinoma,
 CC infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-
 CC Frommel syndrome, Argonz-del Castillo syndrome, Forbes-Albright syndrome,
 CC lymphoma, Shiehnan syndrome or dyszoospermia. The inhibitory agents can
 CC also be used as contraceptives. The agents for modulating placental
 CC function can be used for treating or preventing choriocarcinoma, hydatid
 CC mole, irrigation mole, abortion, untwifity fetus, abnormal
 CC saccharometabolism, abnormal lipidmetabolism or oxytocia
 XX Sequence 31 AA;

Query Match 87.8%; Score 72; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

RESULT 25
 AAY49291 standard; peptide; 31 AA.
 ID AAY49291 standard; peptide; 31 AA.
 XX
 AC AAY49291;
 XX
 DT 22-FEB-2000 (first entry)
 DE 19P2 ligand peptide fragment.
 XX
 KW Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
 KW pituitary; regulatory mechanism; central nervous system; pancreatic.
 XX
 OS Homo sapiens.
 XX
 EH Key Location/Qualifiers
 PT Modified-site 31
 FT /note= "C-terminal amide"
 PN WO960112-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-JP02650.
 XX
 PR 21-MAY-1998; 98JP-00140293.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Matsumoto H, Kitada C, Hiruma S;
 XX
 DR 2000-039381/03.
 XX
 PT New monoclonal antibodies, useful in diagnosis, as drugs and in studying
 PT diseases related to ligand abnormality.
 XX
 PS Disclosure; Page 26; 73pp; Japanese.

The invention provides a monoclonal antibody which has a specific
 CC reaction with the part peptide of the C-terminal of 19P2 ligand or its
 CC derivative. The antibodies can be used in diagnosis or to treat or
 CC prevent diseases associated with abnormality in the pituitary function
 CC regulatory mechanism (e.g. promotion of prolactin secretion), central
 CC nervous regulatory mechanism, and pancreatic function regulatory
 CC mechanism. The antibody-based immunoassay can also be applied in
 CC clarifying the physiological functions of the ligand and its derivative.
 Sequences AAY49291-302 represent peptide fragments of the 19P2 ligand
 XX Sequence 31 AA;

Query Match 87.8%; Score 72; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

RESULT 26
 AAB10362 standard; peptide; 31 AA.
 ID AAB10362 standard; peptide; 31 AA.
 XX
 AC AAB10362;
 XX
 DT 24-NOV-2000 (first entry)
 DE Human oxytocin secretion promoting peptide SEQ ID NO: 32.
 XX
 KW Human; oxytocin secretion promoter; G protein-coupled receptor protein;
 KW treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
 KW caesarean section; artificial fertilization; galactostasis; goat; pig;
 KW veterinary medicine; milk production.
 XX
 OS Homo sapiens.
 XX
 PN WO200038704-A1.
 XX
 AC AAB10362;
 XX
 DT 06-JUL-2000.
 XX
 DE 19P2 ligand peptide fragment.
 XX
 KW Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
 KW pituitary; regulatory mechanism; central nervous system; pancreatic.
 XX
 OS Homo sapiens.
 XX
 EH Key Location/Qualifiers
 PT Modified-site 31
 FT /note= "C-terminal amide"
 PN WO960112-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-JP02650.
 XX
 PR 21-MAY-1998; 98JP-00140293.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Matsumoto H, Kitada C, Hiruma S;
 XX
 DR 2000-039381/03.
 XX
 PT New monoclonal antibodies, useful in diagnosis, as drugs and in studying
 PT diseases related to ligand abnormality.
 XX
 PS Disclosure; Page 26; 73pp; Japanese.

This invention describes a novel oxytocin secretion-regulating agent
 CC which contains a ligand peptide or its salt for the G protein-coupled
 CC receptor protein. It is useful in the form of drugs for ameliorating
 CC preventing and treating diseases relating to oxytocin secretion e.g. weak
 CC pains and atonic bleeding, before and after expulsion of Placenta e.g. weak
 CC uterine recovery failure, caesarean section, stoppage of artificial
 CC fertilization or galactostasis and is also applicable in veterinary
 CC medicine for promoting milk production in cow, goat and pig. This
 CC sequence represents a human peptide which acts as an oxytocin secretion
 CC promoter
 XX Sequence 31 AA;

Query Match 87.8%; Score 72; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

RESULT 27
 AAB0991 standard; peptide; 31 AA.
 ID AAB0991
 XX
 AC AAB0991;
 XX
 DT 22-JUN-2001 (first entry)

DE Prolactin releasing peptide SEQ ID NO:165.
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amine;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200069900-A2.
 XX PD 23-NOV-2000.
 XX PF 17-MAY-2000;
 XX PR 17-MAY-1999;
 XX 99US-0134406P.
 XX PR 10-SEP-1999;
 XX 99US-0153406P.
 XX PR 15-OCT-1999;
 XX 99US-0159783P.
 PA (CONJ-) CONJUCHEM INC.
 XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX WPI; 2001-112059/12.
 XX DR 2001-112059/12.
 XX PS Disclosure; Page 245; 733DP; English.
 XX PR Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX PS Disclosure; Page 244; 733p; English.
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC They are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB9029 to AAB2441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX SQ Sequence 31 AA;
 XX Query Match 87.8%; Score 72; DB 4; Length 31;
 XX Best Local Similarity 100.0%; Pred. No. 2.4e-05;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX RESULT 29
 XX AAG62531
 ID AAG62531 standard; peptide; 31 AA.
 XX AC AAG62531;
 XX DT 24-AUG-2001 (First entry)
 XX DE Human CRH releasing protein related peptide SEQ ID NO: 32.
 XX ID AAG62531
 KW Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;
 KW analgesic; hyperaldostronism; hypercorticosoilaemia; hypoadrenocorticism;
 KW Addison's disease; adrenal gland hyperfunction; obesity.
 XX OS Homo sapiens.
 XX PN WO200135984-A1.
 XX PD 25-MAY-2001.
 XX XX

DE Pro lactin releasing peptide SEQ ID NO:169.
 XX ID AAB90995 standard; peptide; 31 AA.
 XX AC AAB90995;
 XX DT 22-JUN-2001 (first entry)
 DE Pro lactin releasing peptide SEQ ID NO:169.
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX XX

PF	17-NOV-2000; 2000W0-JP008119.	PT	PT antagonist.
XX		XX	Disclosure; Page 24; 35pp; English.
PR	18-NOV-1999; 99JP-00327900.	PS	
XX	26-SEP-2000; 2000JP-00297073.	XX	The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing peptide (PrRP) receptor (GPR10) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. PrRP receptor agonists may be used to treat common disorders which lead to sleepiness, e.g., sleep apnoea, narcolepsy, idiopathic hypersomnia and psychogenic hypersomnia. PrRP receptor antagonists are useful for promoting sleep and for treating insomnia such as adjustment sleep disorder and psychophysiological insomnia. The present sequence is human PrRP-31 peptide.
PA	(TAKE) TAKEDA CHEM IND LTD.	CC	
XX	Kitada C, Matsumoto H, Hinuma S;	CC	
PI	XX	CC	
XX	DR; 2001-355552/37.	CC	
XX	PT	CC	
XX	Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion.	CC	
XX	Claim 3; Page 73-74; 90pp; Japanese.	CC	
PS		CC	
XX	CC	CC	
CC	The present sequence describes a method of controlling the secretion of corticotropin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercorisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypertension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the invention	CC	
SQ	Sequence 31 AA;	CC	
Query Match	87.8%; Score 72; DB 4; Length 31;	XX	Sequence 31 AA;
Best Local Similarity	100.0%; Pred. No. 2.4e-05;	XX	Query Match 87.8%; Score 72; DB 5; Length 31;
Matches	0; Mismatches 0; Indels 0; Gaps 0;	XX	Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Conservative		XX	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC		XX	
DB	2 AWYASRGIRGPVGR 14 18 AWYASRGIRGPVGR 30	XX	
Query Match	87.8%; Score 72; DB 4; Length 31;	RESULT 31	RESULT 31
Best Local Similarity	100.0%; Pred. No. 2.4e-05;	ID	ABU60843
Matches	0; Mismatches 0; Indels 0; Gaps 0;	ID	ABU60843 standard; peptide; 31 AA.
Conservative		XX	
AC		XX	
DB	2 AWYASRGIRGPVGR 14 18 AWYASRGIRGPVGR 30	XX	
Query Match	87.8%; Score 72; DB 4; Length 31;	RESULT 30	RESULT 30
Best Local Similarity	100.0%; Pred. No. 2.4e-05;	ID	AAE26401
Matches	0; Mismatches 0; Indels 0; Gaps 0;	ID	AAE26401 standard; peptide; 31 AA.
Conservative		XX	
AC		XX	
DB	2 AWYASRGIRGPVGR 14 18 AWYASRGIRGPVGR 30	XX	
Query Match	87.8%; Score 72; DB 4; Length 31;	RESULT 30	RESULT 30
Best Local Similarity	100.0%; Pred. No. 2.4e-05;	ID	AAE26401
Matches	0; Mismatches 0; Indels 0; Gaps 0;	ID	AAE26401 standard; peptide; 31 AA.
Conservative		XX	
AC		XX	
DB	2 AWYASRGIRGPVGR 14 18 AWYASRGIRGPVGR 30	XX	
Human PrRP-31 peptide.	XX	XX	
KW	Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;	XX	
KW	PrRP; GPR10; therapy; epilepsy; narcolepsy; sleep apnoea;	XX	
KW	insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;	XX	
KW	anticonvulsant.	XX	
OS	Homo sapiens.	XX	
XX	US2002037533-A1.	XX	
PN		XX	
PD	28-MAR-2002.	DR	WPI; 2003-129302/12.
XX		XX	
PF	17-AUG-2001; 2001US-00932161.	PT	Process for producing peptides e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
XX		PT	
PR	28-APR-2000; 2000US-00560915.	PT	
XX		PT	
PA	(CIVE/) CIVELLI O. (LINS/) LIN S.	PT	
XX		PT	
PI	Civelli O, Lin S;	CC	The invention describes a method of producing a peptide comprising the excision of the N and C-terminal of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, Peptide production can be carried out easily to provide large quantities of the
XX		CC	
DR	WPI; 2002-403931/43.	CC	
XX	Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or	CC	
PT		CC	
PT		CC	

CC required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention

XX
SQ Sequence 31 AA;
Query Match Score 72%; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 AWYASRGIRPVGR 14
Db 18 AWYASRGIRPVGR 30

RESULT 32
ABU60827 ID ABU60827 standard; peptide; 31 AA.
XX
AC ABU60827;
XX DT 06-MAY-2003 (first entry)
XX Peptide production by gene recombination associated peptide #11.
XX Peptide production; low-molecular peptide; Kiss-1; GPR8 ligand;
KW gene recombination.
XX Homo sapiens.
GS WO200292829-A1.
XX PD 21-NOV-2002.
PP 16-MAY-2002; 2002WO-JP004735.
XX PR 17-MAY-2001; 2001JP-00147341.
PA (TAKE) TAKEDA CHEM IND LTD.
PI Nishimura O, Suegaga M, Ito T, Kitada C;
XX DR WPI; 2003-12930/12.
XX PT Process for producing peptides e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
XX Disclosure; Page 59; 87pp; Japanese.

CC The invention describes a method of producing a peptide comprising the CC C-termini of a target peptide with enzymes or CC chemically through the attached cleavage sites repeated by ligation in a CC precursor protein. The method is for producing (low-molecular) peptides CC e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by the CC gene recombination technique through tandem repeats to provide a CC precursor protein with specific cleavage sites. With this method, peptide CC production can be carried out easily to provide large quantities of the CC required peptides. This is the amino acid sequence of a peptide CC associated with the peptide production method of the invention

XX SQ Sequence 31 AA;

Query Match Score 72%; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 AWYASRGIRPVGR 14
Db 18 AWYASRGIRPVGR 30

RESULT 33
ADC71228

ID ADC71228 standard; peptide; 31 AA.
XX
AC ADC71228;
XX DT 18-DEC-2003 (first entry)

XX Human peptide sequence 2 related to the human serine protease.
DE human; serine protease precursor; hormone; neurohypophysial; diabetes;
KW diabetic retinopathy; cataract; antidiabetic; ophthalmological.
XX
OS Homo sapiens.
PN WO2003062429-A1.
XX
PD 31-JUL-2003.
XX
PS 22-JAN-2003; 2003WO-JP000547.
XX
PR 23-JAN-2002; 2002JP-00013549.
XX PR 10-OCT-2002; 2002JP-00298003.
XX PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX PI Kagoshima M, Yamaji N, Takeda M, Abe K, Kawabe T;
XX DR WPI; 2003-598754/56.
XX
PT Protease precursor for developing treatment for diabetes and cataracts.
XX
PS Example 10; SEQ ID NO 13; 61pp; Japanese.

XX This invention relates to a novel human serine protease precursor polypeptide. Specifically, it refers to a novel type II transmembrane serine protease that participates in the control of hormones produced by the pancreatic gland. As such, it can be used in a screening method for the identification of compounds that are useful for the treatment of diseases where a neurohypophysial hormone participates, such as diabetes, diabetic retinopathy and cataract. The present invention describes the compounds of this invention is antidiabetic and ophthalmological. This peptide sequence is human peptide 2 related to the human serine protease of the invention.

XX SQ Sequence 31 AA;
Query Match Score 72%; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 18 AWYASRGIRPVGR 30
RESULT 34
AAW31392 AAW31392 standard; peptide; 32 AA.
ID AAW31392
XX AC AAW31392;
XX DT 06-APR-1998 (first entry)
XX Human type G protein-coupled receptor ligand fragment 2.
DB G protein-coupled receptor; ligand binding; pharmaceutical; modulator;
KW pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
XX OS Homo sapiens.
PN WO9724436-A2.
XX PD 10-JUL-1997.

XX	PF 26-DEC-1996;	95WO-JP003821.	PR 25-DEC-1998;	98JP-00369585.
PR 28-DEC-1995;	95JP-00343371.	XX (TAKE) TAKEDA CHEM IND LTD.	PA	
PR 15-MAR-1996;	95JP-00059419.	XX Mattsumoto H, Kitada C, Hinuma S;	PI	
PR 12-AUG-1996;	95JP-00211805.	XX	XX	
PR 18-SEP-1996;	95JP-00246573.	DR WPI; 2000-452298/39.	XX	
PA (TAKE) TAKEDA CHEM IND LTD.		XX		
XX Hiruma S, Habata Y, Kawamoto Y, Hosoya M, Fujii R, Fukusumi S;		XX Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.	PT	
PI Kitada C;		PT	PT	
XX WPI; 1997-363672/33.		PT	PT	
DR N-PSDB; AAV02429.		XX Disclosure: Page 62; 72pp; Japanese.	PS	
XX Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland.		XX This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery section, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion promoter	CC	
PS Claim 2; Page 185; 258pp; English.		XX DR Sequence 32 AA;	SQ	
XX This sequence represents a peptide fragment from a novel human type CC ligand polypeptide corresponding to amino acid residues 23 to 54 of the CC sequence represented in AAV31390 and is used in an assay to monitor CC ligand binding to the G protein-coupled receptor protein. Pharmaceutical CC compositions containing this ligand may be used as a pituitary function CC modulator, a central nervous system modulator or a pancreatic function CC modulator. This ligand could have specific applications as a prophylactic CC therapeutic agent for dementia, depression, hyperkinetic syndrome, CC growth hormone secretory disease, anxiety syndrome, hypoglycaemia, CC cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, CC rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, CC amyotrophic lateral sclerosis, acute myocardial infarction, infertility, CC spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, CC osteoporosis and/or oligogalactia. Assays can also be developed to screen CC compounds which are capable of altering the binding activity of the CC ligand affecting activation of the G protein-coupled receptor protein	CC			
XX SQ Sequence 32 AA;		XX Query Match 87.8%; Score 72; DB 3; Length 32; Best Local Similarity 100.0%; Pred. No. 2.5e-05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DT	
XX		XX Qy 2 AWYASRGIRPVGR 14	Qy	2 AWYASRGIRPVGR 14
AC AC AAGG2532;		XX Db 18 AWYASRGIRPVGR 30	Db	18 AWYASRGIRPVGR 30
XX		XX RESULT 36 AAGG62532 standard; peptide; 32 AA.	ID	AAGG62532 standard; peptide; 32 AA.
XX		XX ID AAGG2532;	XX	
AC AC AAGG2532;		XX DT 24-AUG-2001 (first entry)	XX	
XX		XX DE Human CRH releasing protein related peptide SEQ ID NO: 33.	DE	
XX		XX KW Human; corticotrophin releasing hormone; CRH; G protein receptor ligand; KW analgesic; hyperaldosteronism; hypertension; hypofunction; Addison's disease; adrenal gland hyperfunction; obesity.	KW	
XX		XX KW Homo sapiens.	OS	
XX		XX XX WO200135984-A1.	XX	
XX		XX PD 25-MAY-2001.	PD	
XX		XX XX 17-NOV-2000; 2000WO-JP008119.	PF	
XX		XX XX 18-NOV-1999; 99JP-00327900.	PR	
XX		XX PR 26-SEP-2000; 2000JP-00297013.	PR	
XX		XX (TAKE) TAKEDA CHEM IND LTD.	PA	
XX		XX PI Kitada C, Matsumoto H, Hinuma S;	PI	
XX		XX DR WPI; 2001-355552/37.	DR	
XX		XX PT Use of G protein receptor ligand or peptide for controlling corticotropin	PT	
XX		XX PT releasing hormone secretion.	PT	
XX		XX Disclosure; Page 74; 90pp; Japanese.	PS	
PP 22-DEC-1999;	99WO-JP007199.			

KW analgesic; hyperaldosteronism; hypercortisolæmia; hypoadrenocorticism;
 KW Addison's disease; adrenal gland hyperfunction; obesity.
 XX Homo sapiens.

RESULT 39
 ID AAB10364 Standard; peptide; 33 AA.
 XX
 AC AAB10364;
 XX DT 24-NOV-2000 (first entry)
 DE Human oxytocin secretion promoting peptide SEQ ID NO: 34.
 KW Human; oxytocin secretion promoter; G protein-coupled receptor protein;
 treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
 caesarean section; artificial fertilization; galactostasis; goat; pig;
 veterinary medicine; milk production.
 XX OS Homo sapiens.
 PN WO200038704-A1.
 XX
 XX 06-JUL-2000.
 PF 22-DRC-1999; 99WO-JP007199.
 XX PR 25-DEC-1998; 98JP-0036585.
 PA (TAKES) TAKEDA CHEM IND LTD.
 XX PI Matsumoto H, Kitada C, Hinuma S;
 DR WPI; 2001-35552/37.
 XX PT Use of G protein receptor ligand or peptide for controlling corticotropin
 PT releasing hormone secretion.
 XX PS Disclosure; Page 74; 90pp; Japanese.
 XX CC The present sequence describes a method of controlling the secretion of
 corticotrophin releasing hormone (CRH), involving the use of a G protein
 receptor ligand. This can be used to control the secretion of CRH and is
 useful as an analgesic or for treating, preventing or ameliorating
 diseases associated with CRH secretion such as hyperaldosteronism,
 CC hypercortisolæmia, secondary or chronic hypoadrenocorticism, Addison's
 CC disease (including boredom, nausea, pigmentation, hypogonadism, hair
 CC loss, and hypotension), adrenal gland hypofunction and obesity. The
 CC present sequence is a peptide used in the exemplification of the
 CC invention
 XX SQ Sequence 33 AA.
 Query Match 87.8%; Score 72; DB 4; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

SEARCH COMPLETED: February 25, 2004, 06:42:35
 Job time : 55 secs

RESULT 40
 ID AAG62533 Standard peptide; 33 AA.
 AC AAG62533;
 XX
 XX 24-AUG-2001 (first entry)
 DE Human CRH releasing protein related peptide SEQ ID NO: 34.
 KW Human; corticotrophin releasing hormone; CRH; G protein receptor ligand;

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OM protein - protein search, using sw model

Run on: February 25, 2004, 06:41:30 ; Search time 23 Seconds
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Title: US-09-700-643A-7
 Perfect score: 82
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 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000 .

Post-processing: Minimum Match 0%
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Database : Issued_Patents_AA:
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 5: /cgn2_6/ptoodata/2/iaa/PCTUS_COMB.pep:
 6: /cgn2_6/ptoodata/2/iaa/backfile1.pep:
 6: /cgn2_6/ptoodata/2/iaa/backfile1.pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	93.9	15	3 US-08-776-971-93	Sequence 93, App1
2	72	87.8	21	3 US-09-105-678A-46	Sequence 46, App1
3	72	87.8	20	3 US-08-776-971-64	Sequence 64, App1
4	72	87.8	20	4 US-09-421-208-46	Sequence 46, App1
5	72	87.8	20	4 US-09-560-915-18	Sequence 18, App1
6	72	87.8	21	3 US-09-105-678A-47	Sequence 47, App1
7	72	87.8	21	3 US-08-776-971-65	Sequence 65, App1
8	72	87.8	21	3 US-09-421-208-47	Sequence 47, App1
9	72	87.8	22	3 US-09-105-678A-48	Sequence 48, App1
10	72	87.8	22	3 US-08-776-971-66	Sequence 66, App1
11	72	87.8	22	3 US-09-421-208-48	Sequence 48, App1
12	72	87.8	31	3 US-09-105-678A-49	Sequence 9, App1
13	72	87.8	31	3 US-09-105-678A-43	Sequence 43, App1
14	72	87.8	31	3 US-08-776-971-61	Sequence 61, App1
15	72	87.8	31	3 US-09-421-208-49	Sequence 49, App1
16	72	87.8	31	3 US-08-776-971-63	Sequence 63, App1
17	72	87.8	31	4 US-09-560-915-15	Sequence 44, App1
18	72	87.8	32	3 US-09-105-678A-44	Sequence 62, App1
19	72	87.8	32	3 US-08-776-971-62	Sequence 44, App1
20	72	87.8	32	3 US-09-421-208-44	Sequence 45, App1
21	72	87.8	33	3 US-09-105-678A-45	Sequence 63, App1
22	72	87.8	33	3 US-08-776-971-63	Sequence 45, App1
23	72	87.8	33	3 US-09-421-208-45	Sequence 59, App1
24	72	87.8	87	3 US-08-776-971-59	Sequence 135, App1
25	72	87.8	87	3 US-08-776-971-135	Sequence 138, App1
26	72	87.8	87	3 US-08-776-971-138	Sequence 30, App1
27	82.9	82.9	19	3 US-09-105-678A-30	Sequence 5, App1

ALIGNMENTS

RESULT 1
 US-08-776-971-93
 / Sequence 93, Application US/08776971.B
 / Patent No. 628934
 / GENERAL INFORMATION:
 / GENERAL APPLICANT: Hiruma, Shuji
 / Habata, Yugo
 / Kawamura, Yuji
 / Hosoya, Masaki
 / Fujii, Ryō
 / Fukusumi, Shoji
 / Kitada, Chieko
 / TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
 / NUMBER OF SEQUENCES: 140
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 / STREET: 130 Water Street
 / CITY: Boston
 / STATE: MA
 / COUNTRY: USA
 / ZIP: 02109
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSeq for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/776,971B
 / FILING DATE: 06-Feb-1997
 / CLASSIFICATION: <Unknown>
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: PCT/JP96/03821
 / FILING DATE: 28-DEC-1996
 / APPLICATION NUMBER: JP 7/343371
 / FILING DATE: 12-AUG-1996
 / APPLICATION NUMBER: JP 8/246573
 / FILING DATE: 28-DEC-1995
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Corlin, David G.
 / REGISTRATION NUMBER: 27,026
 / REFERENCE/DOCKET NUMBER: 47176
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 617-533-3400
 / TELEFAX: 617-533-6440
 / INFORMATION FOR SEQ ID NO: 93:
 / SEQUENCE CHARACTERISTICS:
 /

LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 93:
 US-09-776-971-93

Query Match Best Local Similarity 92.9%; Score 77; DB 3; Length 15;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 CAWYASRGIRPVGR 14
Db	1 CAWZAGRGRIPRVGR 14

RESULT 2

US-09-105-678A-46

Sequence 46, Application US/09105678A
 Patent No. 6103882

GENERAL INFORMATION:
 APPLICANT: Shenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
 ADDRESSSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 27,026
 NAME: Conlin, David G.

REFERENCE/DOCKET NUMBER: 47176
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

SEQUENCE FOR SEQ ID NO: 46:
 US-09-105-678A-46

Query Match Best Local Similarity 100.0%; Score 72; DB 3; Length 20;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2 AWYASRGIRPVGR 14
Db	7 AWYASRGIRPVGR 19

RESULT 4

US-09-421-208-46

Sequence 46, Application US/09421208
 Patent No. 6258561

GENERAL INFORMATION:
 APPLICANT: Shenaga, Masato

APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/421,208
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678
 FILING DATE: 26-JUN-1998
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-421-208-46

Query Match 87.8%; Score 72; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1..e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 5
 US-09-560-915-1B
 FILE REFERENCE: P-UC 3534
 CURRENT APPLICATION NUMBER: US/09/560,915
 i Sequence 1.8, Application US/09560915
 i Patent No. 6383764
 GENERAL INFORMATION:
 i APPLICANT: Civelli, Olivier
 i APPLICANT: Lin, Steven
 i TITLE OF INVENTION: Therapeutic Compositions and Methods
 i TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
 i FILE REFERENCE: P-UC 3534
 i CURRENT FILING DATE: 2000-04-28
 i NUMBER OF SEQ ID NOS: 24
 i SOFTWARE: FastSEQ for Windows Version 4.0
 i SEQ ID NO 18
 i LENGTH: 20
 i TYPE: PR
 i ORGANISM: Homo Sapien
 US-09-560-915-1B

Query Match 87.8%; Score 72; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1..e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 6
 US-09-105-678A-47
 Query Match 87.8%; Score 72; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1..e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 7
 US-08-776-971-65
 Query Match 87.8%; Score 72; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1..e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

GENERAL INFORMATION:
 i APPLICANT: Hinuma, Shuji
 i APPLICANT: Habata, Yugo
 i APPLICANT: Kawamata, Yuji
 i APPLICANT: Hosoya, Masaki
 i APPLICANT: Fujii, Ryō
 i APPLICANT: Fukusumi, Shōji
 i APPLICANT: Kiteda, Chieko
 i TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE

NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,971B
 FILING DATE: 06-Feb-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03821
 FILING DATE: 28-DEC-1996
 APPLICATION NUMBER: JP 7/343371
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 12-AUG-1996
 APPLICATION NUMBER: JP 8/246573
 FILING DATE: 18-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 65:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: Internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 65:
 -08-776-971-65

Best Local Similarity 87.8%; Score 72; DB 3; Length 21;
 SeqMatche 13; Conservative 0; Mismatches 0; Indels 0

Sequence 47, Application US/09421208
 Patent No. 6558561

GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA

TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 48:
 LENGTH: 22 amino acids
 STRANDEDNESS: linear
 TOPOLOGY: Peptide
 MOLECULE TYPE: Peptide
 US-09-105-678A-48

Query Match Score 72; DB 3; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 11
 US-09-421-208-48
 ; Sequence 48, Application US/09421208
 ; Patent No. 625851

GENERAL INFORMATION:
 APPLICANT: Sueenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/421,208
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678
 FILING DATE: 26-JUN-1998
 APPLICATION NUMBER: JP 172118/1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: peptide
 MOLECULE TYPE: peptide
 US-09-421-208-48

Query Match Score 72; DB 3; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYASRGIRPVGR 19

RESULT 12
 US-09-105-678A-9
 ; Sequence 9, Application US/09105678A

Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 PRIORITY DATE: 26-JUN-1998
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678A
 FILING DATE: 26-JUN-1998
 REFERENCE/DOCKET NUMBER: 48466-342
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 PRIORITY DATE: 26-JUN-1998
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-43

Query Match Score 72%; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

RESULT 14
 US-08-776-971-61
 ; Sequence 61, Application US/08776971B
 ; Patent No. 6,228984
 GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 Habata, Yugo
 Kawanata, Yuji
 Hosoya, Masaki
 Fujii, Ryo
 Fukusumi, Shoji
 Kitada, Chieko
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,971B
 FILING DATE: 06-Feb-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03821
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP /343371
 FILING DATE: 15-MAR-1996
 APPLICATION NUMBER: JP 8,59419
 FILING DATE: 12-AUG-1996
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 18-SEP-1996
 APPLICATION NUMBER: JP 8/246573

RESULT 13
 US-09-105-678A-43
 Sequence 43, Application US/09105678A
 Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 61:
 US-08-776-971-61:

Query Match	87.8%	Score 72;	DB 3;	Length 31;
Best Local Similarity	100.0%	Pred. No. 1.8e-05;		
Matches	13;	Conservative	0;	Indels 0;
Gaps	0;			

RESULT 16
 US-09-421-208-43
 Sequence 43, Application US/09421208
 ; Patent No. 6288561
 ; GENERAL INFORMATION:
 ; APPLICANT: Suenaga, Masato
 ; APPLICANT: Moriya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/421,208
 ; FILING DATE: 09-JUN-1997
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/105,678
 ; FILING DATE: 26-JUN-1998
 ; APPLICATION NUMBER: JP 172118/1997
 ; FILING DATE: 27-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Conlin, David G.
 ; REGISTRATION NUMBER: 27,026
 ; REFERENCE/DOCKET NUMBER: 48466-342
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-09-421-208-43

Query Match

87.8%	Score 72;	DB 3;	Length 31;	
Best Local Similarity	100.0%	Pred. No. 1.8e-05;		
Matches	13;	Conservative	0;	Indels 0;
Gaps	0;			

RESULT 17
 US-09-56-915-15
 Sequence 15, Application US/09560915
 ; Patent No. 6383764
 ; GENERAL INFORMATION:
 ; APPLICANT: Civelli, Olivier
 ; APPLICATION: Civelli, Olivier
 ; APPLICANT: Lin, Steven

TITLE OF INVENTION: Therapeutic Compositions and Methods (PrRP)

FILE REFERENCE: P-JC 3534

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 15

LENGTH: 31

TYPE: PRP

ORGANISM: Homo Sapien

US-09-560-915-15

Query Match 87.8%; Score 72; DB 4; Length 31;

Best Local Similarity 100.0%; Prd. No. 1.8e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 18 AWYASRGIRPVGR 30

RESULT 18

US-09-105-678A-44

Sequence 44, Application US/091.05678A

Patent No. 6103812

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

NUMBER OF SEQUENCES: 52

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

CORRESPONDENCE ADDRESS:

ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.3.0

APPLICATION NUMBER: US/09/105,678A

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 47176

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 62:

US-08-776-971-62

Query Match 87.8%; Score 72; DB 3; Length 32;

Best Local Similarity 100.0%; Prd. No. 1.8e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 18 AWYASRGIRPVGR 30

RESULT 20

Query 2 AWYASRGIRPVGR 14

Db 18 AWYASRGIRPVGR 30

US-09-421-208-44

Sequence 44, Application US/09421208
 Patent No. 6255561
 GENERAL INFORMATION:
 APPLICANT: Suenga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIME, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/421,208
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/421,208
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678
 FILING DATE: 26-JUN-1998
 PRIORITY APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-421-208-44

Query Match 87.8% Score 72; DB 3; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

RESULT 22
 US-09-776-971-63
 Sequence 63, Application US/08776971B
 / Sequence No. 622894
 / GENERAL INFORMATION:
 / APPLICANT: Hiruma, Shuji
 / Habata, Yugo
 / Kawamat, Yuji
 / Hosoya, Masaki
 / Fujii, Ryo
 / Fukusumi, Shoji
 / Kitada, Chieko
 / TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
 / NUMBER OF SEQUENCES: 140
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: DIME, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 / STREET: 130 Water Street
 / CITY: Boston
 / STATE: MA
 / COUNTRY: USA
 / ZIP: 02109
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSEQ for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/776,971B
 / FILING DATE: 06-Feb-1997
 / CLASSIFICATION: <Unknown>
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: PCT/JP96/03821
 / FILING DATE: 28-DEC-1996
 / APPLICATION NUMBER: JP 7/343371
 / FILING DATE: 28-DEC-1995
 / APPLICATION NUMBER: JP 8/59419
 / FILING DATE: 15-MAR-1996
 / APPLICATION NUMBER: JP 8/211805

RESULT 21
 US-09-105-678A-45
 Sequence 45, Application US/09105678A
 Patent No. 6103882
 GENERAL INFORMATION:
 APPLICANT: Suenga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIME, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:

FILING DATE: 12-AUG-1996
 APPLICATION NUMBER: JP 8/2446573
 FILING DATE: 18-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 63:
 US-08-776-971-63

Query Match 87.8%; Score 72; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYASRGIRPVGR 30

RESULT 24
 US-08-776-971-59
 Sequence 59, Application US/08776971B
 Patent No. 628984

GENERAL INFORMATION:
 APPLICANT: Hiruma, Shuji
 Habata, Yugo
 Kawamura, Yuji
 Hosoya, Masaki
 Fujii, Ryo
 Fukushima, Shoji
 Kitada, Chieko
 TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASCAL FOR Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,971B
 FILING DATE: 06-Feb-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP96/03821
 FILING DATE: 28-DEC-1996
 APPLICATION NUMBER: JP 7/343371
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 12-AUG-1995
 APPLICATION NUMBER: JP 8/246573
 FILING DATE: 18-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 87 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:
 US-08-776-971-59

Query Match 87.8%; Score 72; DB 3; Length 87;

Best Local Similarity 100.0%; Pred. No. 5.2e-05; Mismatches 0; Indels 0; Gaps 0; Db 40 AWYASRGIRPVGR 52

Qy 2 AWYASRGIRPVGR 14
Db 40 AWYASRGIRPVGR 52

RESULT 25
US-08-776-971-135
Sequence 135, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: PartSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
PRIORITY NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/244573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/244573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 47176
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 138:
US-08-776-971-138

Query Match 87.8%; Score 72; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 5.2e-05; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 40 AWYASRGIRPVGR 52

RESULT 27
US-09-105-678A-30

Sequence 30, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/776,971B

FILING DATE: 06-Feb-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 47176

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: Linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-08-776,971-4

Query Match Score 82.9%; Score 68; DB 3; Length 19;

Best Local Similarity 92.3%; Pred. No. 5e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 29

US-09-421-208-30

Sequence 30, Application US/09421208

Patent No. 6258561.

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,208

FILING DATE:

RESULT 28

US-08-776,971-4

Sequence 4, Application US/08776971B

GENERAL INFORMATION:

Patent No. 6228984

APPLICANT: Hinuma, Shuji

Habata, Yugo

Kawamata, Yuji

Hosoya, Masaki

Fujii, Ryo

Fukusumi, Shoji

Kiteda, Chieko

TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE

NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678
 FILING DATE: 26-JUN-1998
 PRIORITY NUMBER: JP 172118/1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-421-208-30

Query Match 82.9% Score 68; DB 3; Length 19;

Best Local Similarity 92.3%; Pred. No. 5e-05; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASGRGIRPVGR 14

Dy 7 AWYAGRGRIPVGR 19

RESULT 30

US-09-105-678A-34

Patent No. 6103882 Application US/09105678A

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19PB2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B

FILING DATE: 06-Feb-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: JP 27,026

REFERENCE/DOCKET NUMBER: 47176

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-08-776,971-8

US-09-105-678A-34

Query Match 82.9% Score 68; DB 3; Length 20;

Best Local Similarity 92.3%; Pred. No. 5.3e-05; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASGRGIRPVGR 14

Dy 7 AWYAGRGRIPVGR 19

RESULT 31

US-08-776,971-8

Sequence 8, Application US/08776971B

Patent No. 622884

GENERAL INFORMATION:

APPLICANT: Hiruma, Shoji

Kitada, Chieko

Habata, Yugo

Kavamata, Yuji

Hosoya, Masaki

Fujii, Ryo

Fukusumi, Shoji

Kikuchi, Chiaki

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B

FILING DATE: 06-Feb-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REGISTRATION NUMBER: JP 27,026

REFERENCE/DOCKET NUMBER: 47176

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-08-776,971-8

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-08-776,971-8

Qy 2 AWYASRGIRPVGR 14
Db 7 AWYASRGIRPVGR 19

RESULT 32
US-08-776-971-98
Sequence 98, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fuji, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ For Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/3433171
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/594119
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE DOCKET NUMBER: 47176
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 98:

US-08-776-971-98
Query Match 82.9%; Score 68; DB 3; Length 20;
Best Local Similarity 92.3%; Pred. No. 5.0e-05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 7 AWYASRGIRPVGR 19

RESULT 33
US-09-421-208-34
Sequence 34, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Sueanaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Taraka, Yoko
APPLICANT: Niishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentInRelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421-208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3410
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-421-208-34
Query Match 82.9%; Score 68; DB 3; Length 20;
Best Local Similarity 92.3%; Pred. No. 5.3e-05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 7 AWYASRGIRPVGR 19

RESULT 34
US-09-560-915-16
Sequence 16, Application US/09560915
Patent No. 6383764
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/09/560,915
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 20
TYPE: PRT
ORGANISM: Bos taurus

RESULT 35

US-09-560-915-16

Query Match 82.9%; Score 68; DB 4; Length 20;
Best Local Similarity 92.3%; Pred. No. 5.3e-01; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 1;

Qy 2 AWYASRGIRPVGR 14
| ||| | | | | | | |
Db 7 AWYAGRGIRPVGR 19

RESULT 35

US-09-105-678A-35

/ Sequence 35, Application US/09105678A

; GENERAL INFORMATION:

; APPLICANT: Suenaga, Masato

; APPLICANT: Moriya, Takeo

; APPLICANT: Tanaka, Yoko

; APPLICANT: Nishimura, Osamu

; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105, 678A

FILING DATE: 26-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Corlin, David G.

REGISTRATION NUMBER: 27, 026

REFERENCE DOCKET NUMBER: 47176

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLLOGY: Linear

MOLCULE TYPE: peptide

US-09-105-678A-35

Query Match 82.9%; Score 68; DB 3; Length 21;
Best Local Similarity 92.3%; Pred. No. 5.5e-05; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 1;

Qy 2 AWYASRGIRPVGR 14
| ||| | | | | | | |
Db 7 AWYAGRGIRPVGR 19

RESULT 36

US-09-421-208-35

/ Sequence 35, Application US/09421208

; GENERAL INFORMATION:

; APPLICANT: Suenaga, Masato

; APPLICANT: Moriya, Takeo

; APPLICANT: Taraka, Yoko

; APPLICANT: Nishimura, Osamu

; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/421,208
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678
 FILING DATE: 26-JUN-1998
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 48466-342
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEX/FAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-105-678A-36

Query Match 82.9%; Score 68; DB 3; Length 21;
 Best Local Similarity 92.3%; Pred. No. 5.5e-05;
 Matches 12; Conservative 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
 Db 7 AWYAGRGIRPVGR 19

RESULT 39
 US-08-776-971-10

Sequence 10, Application US/08776971B
 Patent No. 6228984

GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 Habata, Yugo
 Kawamata, Yuji
 Fujii, Ryō
 Hosoya, Masaki

TITLE OF INVENTION: PROTEINS, THEIR PRODUCTION AND USE
 NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA

COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,971B
 FILING DATE: 06-Feb-1997
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/03821
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP 7/343371
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 12-AUG-1996
 APPLICATION NUMBER: JP 8/246573
 FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEX/FAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 FRAGMENT DESCRIPTION: SEQ ID NO: 10:
 US-08-776 971-10

Query Match Score 68; DB 3; Length 22;
 Best Local Similarity 92.3%; Pred. No. 5.8e-05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AWYASRGIRPVGR 14
 Db 7 AWYAGRGRGPVGR 19

RESULT 40
 US-09-421-208-36
 Sequence 36, Application US/09421208
 Patent No. 6258561

GENERAL INFORMATION:
 APPLICANT: Suenaga, Masato
 APPLICANT: Moriya, Takeo
 APPLICANT: Tanaka, Yoko
 APPLICANT: Nishimura, Osamu
 TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/421,208
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/105,678
 FILING DATE: 26-JUN-1998
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

Query Match Score 68; DB 3; Length 22;
 Best Local Similarity 92.3%; Pred. No. 5.8e-05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AWYASRGIRPVGR 14
 Db 7 AWYAGRGRGPVGR 19



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CM protein - protein search, using sw model

Run on: February 25, 2004, 06:43:56 ; Search time 34 Seconds
(without alignments)
93.156 Million cell updates/sec

Title: US-09-700-643A-7

Perfect score: 82

Sequence: 1 CAAWASRGIRPVGRX 15

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Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
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2	72	87.8	20	14	US-10-096-777-18	Sequence 18, Appl
3	72	87.8	31	9	US-10-932-161-15	Sequence 15, Appl
4	72	87.8	31	14	US-10-096-777-15	Sequence 92, Appl
5	87.8	87	13	13	US-10-094-592-92	Sequence 27, Appl
6	82.9	82.9	19	13	US-10-094-592-27	Sequence 16, Appl
7	68	82.9	20	13	US-09-932-161-16	Sequence 42, Appl
8	68	82.9	20	13	US-10-094-592-42	Sequence 16, Appl
9	68	82.9	20	14	US-10-096-777-16	Sequence 43, Appl
10	68	82.9	21	13	US-10-094-592-43	Sequence 44, Appl
11	68	82.9	22	13	US-10-094-592-44	Sequence 13, Appl
12	68	82.9	31	9	US-09-932-161-13	Sequence 39, Appl
13	68	82.9	31	14	US-10-096-777-13	Sequence 13, Appl
14	68	82.9	32	13	US-10-094-592-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
 ; Sequence 18, Application US/09932161
 ; Patent No. US20020037533A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Civelli, Olivier
 ; ATTORNEY: Lin, Steven
 ; TITLE OF INVENTION: Screening and Therapeutic Methods For
 ; Title of Invention: Promoting Wakefulness and Sleep
 ; Title Reference: P-UC 4679
 ; Current Application Number: US/09/932-161
 ; Current Filing Date: 2001-08-17
 ; Prior Application Number: US 09/560,915
 ; Prior Filing Date: 2000-04-28
 ; Number of SEQ ID NOS: 24
 ; Software: FastSQL for Windows Version 4.0
 ; SEQ ID NO: 18
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-932-161-18

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; TITLE OF INVENTION: Therapeutic Compositions and Methods
; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrPr)
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/10/096,777
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 18
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-777-18

RESULT 5
US-10-044-592-92
; Sequence 92, Application US/100444592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hiruma, Shuji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIORITY NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-05-10
; PRIORITY APPLICATION NUMBER: PCT/JP98/01923
; FILE REFERENCE: 246US2P
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO: 92
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-592-92

Query Match 87.8%; Score 72; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e-05; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 18 AWYASRGIRPVGR 30

; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Promoting Wakefulness and Sleep
; FILE REFERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: US/09/932,161
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 09/560,915
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-932-161-15

RESULT 3
US-09-932-161-15
; Sequence 15, Application US/09932161
; Patent No. US2002031533A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Promoting Wakefulness and Sleep
; FILE REFERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: US/09/932,161
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 09/560,915
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-932-161-15

Query Match 87.8%; Score 72; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.2e-05; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 18 AWYASRGIRPVGR 30

; TITLE OF INVENTION: Therapeutic Compositions and Methods
; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrPr)
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/10/096,777
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-27

RESULT 6
US-10-044-592-27
; Sequence 27, Application US/100444592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hiruma, Shuji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; CURRENT APPLICATION NUMBER: 246US2P
; CURRENT FILING DATE: 2002-01-10
; PRIORITY NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-05-10
; PRIORITY APPLICATION NUMBER: PCT/JP98/01923
; FILE REFERENCE: 246US2P
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO: 27
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-27

Query Match 87.8%; Score 72; DB 13; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.00024; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 40 AWYASRGIRPVGR 52

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Best Local Similarity 92.3%; Pred. No. 0.00026; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 9
US-10-096-777-16 ; Sequence 16, Application US/10096777
; Publication No. US200301712701
; GENERAL INFORMATION:
; APPLICANT: Civelli, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Therapeutic Compositions and Methods Relating To Prolactin Releasing Peptide (PrRP)
; FILE REFERENCE: P-JC 3534
; CURRENT APPLICATION NUMBER: US/10/096,777
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-096-777-16

Query Match 82.9%; Score 68; DB 14; Length 20;
Best Local Similarity 92.3%; Pred. No. 0.00028; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 7 AWYAGRGIRPVGR 19

RESULT 10
US-10-044-592-43 ; Sequence 43, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hiruma, Shuji
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 246JUS2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 43
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-43

Query Match 82.9%; Score 68; DB 13; Length 21;
Best Local Similarity 92.3%; Pred. No. 0.00029; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 7 AWYAGRGIRPVGR 19

RESULT 11
US-10-044-592-44 ; Sequence 44, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hiruma, Shuji
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use

Query Match 82.9%; Score 68; DB 13; Length 20;
Best Local Similarity 92.3%; Pred. No. 0.00028; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 7 AWYAGRGIRPVGR 19

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FILE REFERENCE: 2433US2P
// CURRENT APPLICATION NUMBER: US/10/044,592
// CURRENT FILING DATE: 2002-01-10
// PRIOR APPLICATION NUMBER: US 09/403639
// PRIOR FILING DATE: 1999-25-10
// PRIOR APPLICATION NUMBER: PCT/JP98/01923
// PRIOR FILING DATE: 1998-04-27
// PRIOR APPLICATION NUMBER: JP 9-109974
// NUMBER OF SEQ ID NOS: 96
// SEQ ID NO: 44
// LENGTH: 22
// TYPE: PRT
// ORGANISM: Bovine
JUS-10-044-592-44

Query Match 82.9%; Score 68; DB 13; Length 22;
Best Local Similarity 92.3%; Pred. No. 0.0003; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RESULT 12
US 09-932-161-13
// Sequence 13, Application US/09932161
// Patent No. US20020031533A1
GENERAL INFORMATION:
// APPLICANT: Civelli, Olivier
// INVENTION: Screening and Therapeutic Methods For
// TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERENCE: P-UC 46/9
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-04-28
SOFTWARE: FastSEQ For Windows Version 4.0
SEQ ID NO: 13
TYPE: PRT
ORGANISM: Bos taurus
JUS-09-932-161-13

Query Match 82.9%; Score 68; DB 9; Length 31;
Best Local Similarity 92.3%; Pred. No. 0.00042; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RESULT 13
US-10-044-592-39
// Sequence 39, Application US/10044592
// Publication No. US2002143152A1
GENERAL INFORMATION:
// APPLICANT: Hiruma, Shuji
// INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2433US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: JP 9-109974
// NUMBER OF SEQ ID NOS: 96
// SOFTWARE:
// SEQ ID NO: 40
// LENGTH: 32
// TYPE: PRT
// ORGANISM: Bovine
US-10-044-592-40

Query Match 82.9%; Score 68; DB 13; Length 31;
Best Local Similarity 92.3%; Pred. No. 0.00042;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ANYASRGIRPVGR 14
Db 18 ANYAGRGPVGR 30
RESULT 14
US-10-096-777-13
// Sequence 13, Application US/10096777
// Publication No. US20030171270A1
GENERAL INFORMATION:
// APPLICANT: Civelli, Olivier
// INVENTION: Therapeutic Compositions and Methods
// Relating To Prolactin Releasing Peptide (PrRP)
FILE REFERENCE: P-UC 33/4
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2000-03-12
PRIOR APPLICATION NUMBER: US/09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 13
LENGTH: 31
TYPE: PRT
ORGANISM: Bos taurus
US-10-096-777-13

Query Match 82.9%; Score 68; DB 14; Length 31;
Best Local Similarity 92.3%; Pred. No. 0.00042;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ANYASRGIRPVGR 14
Db 18 ANYAGRGPVGR 30
RESULT 15
US-10-044-592-40
// Sequence 40, Application US/10044592
// Publication No. US2002043152A1
GENERAL INFORMATION:
// APPLICANT: Hiruma, Shuji
// INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2433US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: JP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
// SOFTWARE:
// SEQ ID NO: 40
// LENGTH: 32
// TYPE: PRT
// ORGANISM: Bovine
US-10-044-592-40

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Query Match 82.9%; Score 68; DB 13; Length 32;
Best Local Similarity 92.3%; Pred. No. 0.00043;
Matches 12; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 18 AWYAGRGIRPVGR 30

RESULT 16
US-10-044-592-41
; Sequence 41, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hiruma, Shuji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 246-US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIORITY FILING DATE: 2002-01-10
; PRIORITY APPLICATION NUMBER: US 09/403639
; PRIORITY FILING DATE: 1999-04-27
; PRIORITY APPLICATION NUMBER: JP 9-109974
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO: 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-41

Query Match 82.9%; Score 68; DB 13; Length 32;
Best Local Similarity 92.3%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 18 AWYAGRGIRPVGR 30

RESULT 17
US-10-044-592-28
; Sequence 28, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hiruma, Shuji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 246-US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIORITY FILING DATE: 2002-01-10
; PRIORITY APPLICATION NUMBER: US 09/403639
; PRIORITY FILING DATE: 1999-04-27
; PRIORITY APPLICATION NUMBER: JP 9-109974
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO: 28
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Marine
US-10-044-592-28

Query Match 82.9%; Score 68; DB 13; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 40 AWYAGRGIREVGR 52

Query Match 82.9%; Score 68; DB 13; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 40 AWYAGRGIREVGR 52

RESULT 18
US-10-044-592-38
; Sequence 38, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 246-US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIORITY FILING DATE: 1999-04-27
; PRIORITY APPLICATION NUMBER: PC/T/JP98/01923
; PRIORITY FILING DATE: 1998-04-27
; PRIORITY APPLICATION NUMBER: JP 9-109974
; PRIORITY FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO: 38
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-38

Query Match 82.9%; Score 68; DB 13; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 40 AWYAGRGIREVGR 52

RESULT 19
US-10-044-592-82
; Sequence 82, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 246-US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIORITY FILING DATE: 1999-04-27
; PRIORITY APPLICATION NUMBER: PC/T/JP98/01923
; PRIORITY FILING DATE: 1998-04-27
; PRIORITY FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO: 82
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-82

Query Match 82.9%; Score 68; DB 13; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Db 40 AWYAGRGIREVGR 52

LOCATION: (1). (31)
 OTHER INFORMATION: antigen
 US-10-044-592-5

Query Match 78.0%; Score 64; DB 13; Length 31;
 Best Local Similarity 84.6%; Pred. No. 0.0019; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 2;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYTGGIRPVGR 30

RESULT 31
 US-10-096-777-14
 ; Sequence 14, Application US/10096777
 ; Publication No. US20010171270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Civelli, Olivier
 ; LINN, Steven
 ; TITLE OF INVENTION: Therapeutic Compositions and Methods
 ; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRP)
 ; FILE REFERENCE: P-UC 3534
 ; CURRENT APPLICATION NUMBER: US/10/096,777
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: US/09/560,915
 ; PRIOR FILING DATE: 2000-04-28
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 14
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Rattus
 US-10-096-777-14

Query Match 78.0%; Score 64; DB 13; Length 31;
 Best Local Similarity 84.6%; Pred. No. 0.0019; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 2;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYTGGIRPVGR 30

RESULT 32
 US-10-044-592-96
 ; Sequence 96, Application US/10044592
 ; Publication No. US20020143152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fukusumi, Shoji
 ; TITLE OF INVENTION: Polypeptides, their Production and Use
 ; FILE REFERENCE: 2463US2P
 ; CURRENT APPLICATION NUMBER: US/10/044,592
 ; CURRENT FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: US 09/403639
 ; PRIOR FILING DATE: 1999-04-27
 ; PRIOR APPLICATION NUMBER: PCT/JP98/01923
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: JP 9-109974
 ; PRIOR FILING DATE: 1997-04-28
 ; NUMBER OF SEQ ID NOS: 96
 ; SEQ ID NO: 96
 ; LENGTH: 86
 ; TYPE: PRT
 ; ORGANISM: mammalian
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1224)..(1243)
 ; OTHER INFORMATION: Bracket region depicted in FIG 39.

Query Match 78.0%; Score 64; DB 13; Length 70;
 Best Local Similarity 84.6%; Pred. No. 0.004; Indels 2; Gaps 0;
 Matches 11; Conservative 0; Mismatches 2;

Qy 2 AWYASRGIRPVGR 14
 Db 18 AWYTGGIRPVGR 30

```

Db      ||| ||||| 39 AWYTGGRGPRVGR 51
Db      39 AWYTGGRGPRVGR 51

RESULT 33
US-10-044-592-94
; Sequence 94, Application US/10044592
; Publication No. US20143152A1
; GENERAL INFORMATION:
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-04-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: SEQ ID NO: 94
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Mammalian
; FEATURE: misc_feature
; LOCATION: (1) .(31)
; OTHER INFORMATION: primer
; NAME/KEY: misc_feature
; LOCATION: (925) .(955)
; OTHER INFORMATION: primer
; NAME/KEY: misc_feature
; LOCATION: (1) .(955)
; OTHER INFORMATION: primer
; LOCATION: (1) .(955)
; OTHER INFORMATION: insert fragment of pmGB3 as depicted in FIG 36 and 37.
US-10-044-592-94

Query Match      76.0% ; Score 64; DB 13; Length 91;
Best Local Similarity 84.6%; Pred. No. 0.005; Matches 11; Conservative 0; Indels 0; Gaps 0;
Qy      2 AWYASRGGRGPRVGR 14
Db      39 AWYTGGRGPRVGR 51

RESULT 34
US-10-044-592-26
; Sequence 26, Application US/10044592
; Publication No. US20143152A1
; GENERAL INFORMATION:
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-04-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO: 26
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-26

Query Match      76.8%; Score 63; DB 13; Length 29;
Best Local Similarity 91.7%; Pred. No. 0.0026; Matches 11; Conservative 0; Indels 1; Gaps 0;
Qy      2 AWYASRGGRGPRVGR 13
Db      18 AWYTGGRGPRVGR 29

RESULT 35
US-10-044-592-78
; Sequence 78, Application US/10044592
; Publication No. US20143152A1
; GENERAL INFORMATION:
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-04-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO: 78
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Bovine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) .(20)
; OTHER INFORMATION: primer
; NAME/KEY: misc_feature
; LOCATION: (52) .(76)
; OTHER INFORMATION: primer
US-10-044-592-78

Query Match      64.6%; Score 53; DB 13; Length 25;
Best Local Similarity 90.0%; Pred. No. 0.035; Matches 9; Conservative 0; Indels 1; Gaps 0;
Qy      2 AWYASRGGRGPR 11
Db      16 AWYTGGRGPR 25

RESULT 36
US-10-093-463-188
; Sequence 188, Application US/10093463
; Publication No. US20030208039A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Sheroy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Gusev, Vladimir
; APPLICANT: Pochart, Pascal
; APPLICANT: Zhong, Mei
; APPLICANT: Raselli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glenda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Ganguli, Esha
; APPLICANT: Vernet, Corinne
US-10-093-463-188

```

1 / APPLICANT: Pena, Carol
 1 / APPLICANT: Burgess, Catherine
 1 / APPLICANT: Liu, Xiaohong
 1 / APPLICANT: Spytek, Kimberly
 1 / APPLICANT: Gorman, Linda
 1 / APPLICANT: Spaderna, Steven
 1 / APPLICANT: Voss, Edward
 1 / APPLICANT: Malvankar, Uriel
 1 / APPLICANT: Anderson, David
 1 / APPLICANT: Miller, Charles
 1 / APPLICANT: Taurier, Raymond J. Jr.
 1 / TITLE OF INVENTION: No. US20030208039A1 [Antibodies that Bind to Antigenic Polypeptides Encoding The Antigens, and Methods of Use.]
 1 / FILE REFERENCE: 21402-290A (Cura 590AT)
 1 / CURRENT FILING DATE: 2002-06-24
 1 / PRIOR APPLICATION NUMBER: 60/283,675
 1 / PRIOR FILING DATE: 2001-04-14
 1 / PRIOR APPLICATION NUMBER: 60/338,092
 1 / PRIOR FILING DATE: 2001-12-03
 1 / PRIOR APPLICATION NUMBER: 60/274,281
 1 / PRIOR FILING DATE: 2001-03-08
 1 / PRIOR APPLICATION NUMBER: 60/274,101
 1 / PRIOR FILING DATE: 2001-03-08
 1 / PRIOR APPLICATION NUMBER: 60/225,681
 1 / PRIOR FILING DATE: 2001-09-27
 1 / PRIOR APPLICATION NUMBER: 60/304,354
 1 / PRIOR FILING DATE: 2001-07-10
 1 / PRIOR APPLICATION NUMBER: 60/279,995
 1 / PRIOR FILING DATE: 2001-03-30
 1 / PRIOR APPLICATION NUMBER: 60/294,899
 1 / PRIOR FILING DATE: 2001-05-31
 1 / PRIOR APPLICATION NUMBER: 60/287,424
 1 / PRIOR FILING DATE: 2001-04-30
 1 / PRIOR FILING DATE: 2001-06-18
 1 / PRIOR APPLICATION NUMBER: 60/309,198
 1 / PRIOR FILING DATE: 2001-07-31
 1 / PRIOR APPLICATION NUMBER: 60/281,194
 1 / PRIOR FILING DATE: 2001-04-04
 1 / PRIOR APPLICATION NUMBER: 60/274,194
 1 / PRIOR FILING DATE: 2001-03-08
 1 / PRIOR APPLICATION NUMBER: 60/274,849
 1 / PRIOR FILING DATE: 2001-03-09
 1 / PRIOR APPLICATION NUMBER: 60/330,380
 1 / PRIOR FILING DATE: 2001-10-18
 1 / PRIOR APPLICATION NUMBER: 60/275,235
 1 / PRIOR FILING DATE: 2001-03-12
 1 / PRIOR FILING DATE: 2001-05-03
 1 / PRIOR APPLICATION NUMBER: 60/275,578
 1 / PRIOR FILING DATE: 2001-03-13
 1 / NUMBER OF SEQ ID NOS: 370
 1 / SOFTWARE: PatentIn Ver. 2.1
 1 / SEQ ID NO: 188
 1 / LENGTH: 647
 1 / TYPE: PRT
 1 / ORGANISM: Homo sapiens
 us-10-093-463-188
 1 / Query Match Score: 46 / DB 15; Length: 647;
 1 / Best Local Similarity: 64.3%; Pred. No. 27; Mismatches: 4; Indels: 0; Gaps: 0;
 Qy 1 CAWWASRGGRGPVGR 14
 Db 611 CAWGARGRPVPGGR 624
 RESULT 39
 US-10-156 761-10748
 ; Sequence 10748, Application US/10156761
 ; Publication No. US20030113018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI

1 / Publication No. US20030233675A1
 1 / GENERAL INFORMATION:
 1 / APPLICANT: Cao, Yongwei
 1 / APPLICANT: Hinkle, Gregory J.
 1 / APPLICANT: Slater, Steven C.
 1 / APPLICANT: Goldman, Barry S.
 1 / APPLICANT: Chen, Xianfeng
 1 / TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 1 / FILE REFERENCE: 38-10 (5205) B
 1 / CURRENT APPLICATION NUMBER: US/10/369,493
 1 / PRIOR APPLICATION NUMBER: 2003-02-28
 1 / PRIOR FILING DATE: 2002-02-21
 1 / NUMBER OF SEQ ID NOS: 47374
 1 / SEQ ID NO: 12239
 1 / LENGTH: 411
 1 / TYPE: PRT
 1 / ORGANISM: Aspergillus nidulans
 1 / FEATURE:
 1 / NAME/KEY: unsure
 1 / LOCATION: (1). (411)
 1 / OTHER INFORMATION: unsure at all Xaa locations
 US-10-369-493-12939

Qy 2 AWYASSGIRPVGR 14
 Db 281 AWAESHLRPIAR 293
 RESULT 38
 US-10-369-493-8457
 ; Sequence 8457, Application US/10369493
 1 / Publication No. US20030233675A1
 1 / GENERAL INFORMATION:
 1 / APPLICANT: Cao, Yongwei
 1 / APPLICANT: Hinkle, Gregory J.
 1 / APPLICANT: Slater, Steven C.
 1 / APPLICANT: Goldman, Barry S.
 1 / APPLICANT: Chen, Xianfeng
 1 / TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 1 / FILE REFERENCE: 38-10 (5205) B
 1 / CURRENT APPLICATION NUMBER: US/10/369,493
 1 / PRIOR APPLICATION NUMBER: US 60/360,039
 1 / PRIOR FILING DATE: 2003-02-28
 1 / NUMBER OF SEQ ID NOS: 47374
 1 / SEQ ID NO: 8457
 1 / LENGTH: 555
 1 / TYPE: PRT
 1 / ORGANISM: Ralstonia metallidurans
 US-10-369-493-8457

Qy 2 AWYASSGIRPVGR 14
 Db 59 AWLQSRGLRGEAR 71
 RESULT 39
 US-10-156 761-10748
 ; Sequence 10748, Application US/10156761
 ; Publication No. US20030113018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI

RESULT 37
 US-10-369-493-12939
 ; Sequence 12939, Application US/10369493

APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIIKU
 APPLICANT: HATTORI, MASAHIRO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 PRIORITY APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIORITY APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 10748
 LENGTH: 402
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-10748

Query Match 52.4%; Score 43; DB 14; Length 402;
 Best Local Similarity 47.4%; Pred. No. 53; Indels 8; Gaps 1;
 Matches 9; Conservative 1; Mismatches 1;

Qy	3 WYASRG-----IRPG 13
Db	91 WYAPRGQISLRAEIRPG 109

RESULT 40
 US-10-156-761-14927
 Sequence 14927, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIIKU
 APPLICANT: HATTORI, MASAHIRO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 PRIORITY APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIORITY APPLICATION NUMBER: JP 2001-272697
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 14927
 LENGTH: 592
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-14927

Query Match 52.4%; Score 43; DB 14; Length 592;
 Best Local Similarity 72.7%; Pred. No. 76; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 2;

Qy	2 AWYASRGIRPV 12
Db	103 AWMABGRPV 113

Search completed: February 25, 2004, 06:49:23
 Job time : 35 secs



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OM protein - protein search, using sw model

Run on: February 25, 2004, 06:40:45 ; Search time 21 Seconds

(without alignments)
68.708 Million cell updates/sec

Title: US-09-700-643A-7

Perfect score: 82

Sequence: 1 CAWYASRGIRPVGRX 15

Scoring table: BL0SUM62

GapOp 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1		64	78.0	83	2	prolactin-releasing peptide - rat
2		44	53.7	302	2	hypothetical prote
3		44	53.7	719	2	ARPL Protein - Yea
4		42	51.2	105	2	hypothetical prote
5		42	51.2	105	2	hypothetical prote
6		42	51.2	113	2	hypothetical prote
7		42	51.2	132	2	protein-export mem
8		42	51.2	250	2	hypothetical prote
9		42	51.2	269	2	lipid2 protein [imp
10		42	51.2	269	2	hypothetical prote
11		41	50.0	256	2	hypothetical prote
12		41	50.0	276	2	hypothetical prote
13		41	50.0	546	2	hypothetical prote
14		41	50.0	966	2	trwC protein - Erc
15		40.5	49.4	313	2	VirB6 type IV secr
16		40	48.8	267	2	hypothetical prote
17		40	48.8	398	2	acetate kinase - D
18		40	48.8	580	2	AEP2 protein - Yea
19		40	48.8	788	2	recombination prot
20		40	48.8	790	2	hypothetical prote
21		39	47.6	171	2	probable acetyltransferase
22		39	47.6	181	2	hypothetical prote
23		39	47.6	184	2	probable membrane
24		39	47.6	260	2	hypothetical prote
25		39	47.6	315	2	formamidopyrimidin
26		39	47.6	333	2	hydroxybenzoate oc
27		39	47.6	374	2	hypothetical prote
28		39	47.6	424	2	sAMB protein - Sal
29		39	47.6	424	2	UV protection prot

C;superfamily: Mycobacterium tuberculosis hypothetical protein Rv0428c

30	39	47.6	452	1	JNEGCT
31	39	47.6	452	2	E91019
32	39	47.6	452	2	G8863
33	39	47.6	459	2	T45558
34	39	47.6	600	2	D84258
35	39	47.6	2870	2	A3548
36	38	46.3	121	2	H72507
37	38	46.3	194	2	T42347
38	38	46.3	238	2	H72446
39	38	46.3	284	2	F95120
40	38	46.3	294	2	S68784
41	38	46.3	306	1	CPBDB
42	38	46.3	330	2	T42347
43	38	46.3	343	2	E95986
44	38	46.3	416	1	A42332
45	38	46.3	456	2	F90576

ALIGNMENTS

RESULT 1					
JCT7607					
prolactin-releasing peptide - rat					
C;Species: Rattus norvegicus (Norway rat)					
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001					
C;Accession: JC7607					
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Hosoya, T.					
Biochem. Biophys. Res. Commun. 281, 53-56, 2001					
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: Mul					
A;Reference number: JCT7607; PMID:21092785; PMID:1178959					
A;Contents: spleen					
A;Accession: JC7607					
A;Molecule type: DNA					
A;Residues: 1-83 <YAM>					
QY					
2 AWYASGRGIRPVGR 14					
Db					
39 AWYTGGRGIRPVGR 51					
RESULT 2					
B70631					
hypothetical protein Rv0428c - Mycobacterium tuberculosis (strain H37RV)					
C;Species: Mycobacterium tuberculosis					
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000					
C;Accession: B70631					
R;Cole, S.T.; Broich, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.					
Connor, R.; Davies, R.; Devlin, K.; Rutter, S.; Gentles, S.; Hamlin, N.; Holroyd, S.					
Raftandrem, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.					
Nature 393, 537-544, 1998					
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.					
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome					
A;Reference number: A70500; PMID:98295987; PMID:9634230					
A;Accession: B70631					
A>Status: preliminary; nucleic acid sequence not shown; translation not shown					
A;Molecule type: DNA					
A;Residues: 1-302 <COL>					
A;Cross references: GB:Z84724; GB:AU123456; NID:93261708; PMID:CA006568.1; PMID:91817694					
A;Experimental source: strain H37RV					
C;Genetics:					
C;Gene: Rv0428c					
C;superfamily: Mycobacterium tuberculosis hypothetical protein Rv0428c					

Query Match 53.7%; Score 44; DB 2; Length 302;
 Best Local Similarity 70.0%; Pred. No. 8.6;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 A;Gene: AGR_C_2196
 A;Map position: circular chromosome

Qy 2 AWYASRGIRP 11
 Db 126 AWYASRDQGP 135

RESULT 3
 S6.046
 ARPI protein - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: protein YDL17c
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
 C;Accession: S61045; S31139; S67719
 R;Pohl, T.M.
 submitted to the EMBL Data Library, November 1995
 A;Reference number: S61010
 A;Accession: S61046
 A;Molecule type: DNA
 A;Cross-references: EMLB:267750; PIDN:91061256; PIDN:CAA91579.1; PID:gi1061272
 R;Nehner, E.P.; Reio, E.; Brandel, M.
 Mol. Cell. Genet. 237, 351-358, 1993
 A;Title: Molecular structure and genetic regulation of SPA, a gene responsible for resistance to the EMBL Data Library, August 1992
 A;Reference number: S31138; MUID:93247548; PMID:8433449
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Cross-references: EMLB:X65020; PID:9577609; PIDN:CAA48159.1; PID:g288590
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 R;Pohl, T.M.
 submitted to the Protein Sequence Database, July 1996
 A;Reference number: S67708
 A;Accession: S67719
 A;Molecule type: DNA
 A;Cross-references: EMLB:Z74215; PID:91431265; PIDN:CAA98741.1; PID:gi143126
 A;Experimental source: strain S288C
 C;Genetics:
 A;Gene: SGD:NRP1; ARP1
 A;Cross-references: MIPS:YDL167C; SGD:S0002326
 A;Map position: 4L

RESULT 4
 A97505
 hypothetical protein AGR_C_2196 [Imported] - Agrobacterium tumefaciens (strain C58, Cere
 C;Species: Agrobacterium tumefaciens
 C;Accession: A97505
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quroollo, B.; Goldman, R.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Marzelz, B.; Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A;Reference number: A97359; MUID:2160551; PMID:11743194
 A;Accession: A97505
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-105 <KUR>
 A;Cross-references: GB:AE007869; PIDN:AAK86994.1; PID:g15156234; GSPDB:GN00169
 C;Genetics:

Query Match 53.7%; Score 44; DB 2; Length 719;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 A;Gene: AGR_C_2196
 A;Map position: circular chromosome

Qy 2 AWYASRGIRP 13
 Db 244 SWFTQGVPGVPG 255

RESULT 5
 AE2723
 hypothetical protein Atull191 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C;Accession: AE2723
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
 erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyaviv, T.; Levy, R.; Li, M.; McClell
 ; Kartp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 Peter, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:2160550; PMID:11743193
 A;Accession: AE2723
 A;Molecule type: DNA
 A;Residues: 1-105 <KUR>
 A;Cross-references: GB:AB000688; PIDN:AAU42203.1; PID:g1773955; GSPDB:GN00186
 A;Experimental source: strain C58 (Dupont)
 A;Genetic:
 A;Map position: circular chromosome

Query Match 51.2%; Score 42; DB 2; Length 105;
 Best Local Similarity 67.7%; Pred. No. 6.8;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 A;Gene: Atull191
 A;Molecule type: DNA
 A;Residues: 1-105 <KUR>
 A;Cross-references: GB:AB000688; PIDN:AAU42203.1; PID:g1773955; GSPDB:GN00186
 A;Experimental source: strain C58 (Dupont)
 A;Genetic:
 A;Map position: circular chromosome

Query Match 51.2%; Score 42; DB 2; Length 105;
 Best Local Similarity 67.7%; Pred. No. 6.8;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 A;Gene: Atull191
 A;Molecule type: DNA
 A;Residues: 1-105 <KUR>
 A;Cross-references: GB:AB000688; PIDN:AAU42203.1; PID:g1773955; GSPDB:GN00186
 A;Experimental source: strain C58 (Dupont)
 A;Genetic:
 A;Map position: circular chromosome

Query Match 51.2%; Score 42; DB 2; Length 105;
 Best Local Similarity 67.7%; Pred. No. 6.8;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 A;Gene: Atull191
 A;Molecule type: DNA
 A;Residues: 1-105 <KUR>
 A;Cross-references: GB:AB000688; PIDN:AAU42203.1; PID:g1773955; GSPDB:GN00186
 A;Experimental source: strain C58 (Dupont)
 A;Genetic:
 A;Map position: circular chromosome

Query Match 51.2%; Score 42; DB 2; Length 113;
 Best Local Similarity 70.0%; Pred. No. 7.3;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 A;Gene: ar7057
 A;Genome: plasmid

Query Match 51.2%; Score 42; DB 2; Length 113;
 Best Local Similarity 70.0%; Pred. No. 7.3;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 64 ANYAKAGIEP 73

Db 237 CAEBOLRALRPG 249

RESULT 7
 BB2824 protein-export membrane protein XFO304 [imported] - *Xylella fastidiosa* (strain 95c)

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: BB2824

R;anonymous. The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen-

ce Network 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MUID:10910347

A;Note: For complete list of authors see reference number A59328 below

A;Accession: BB2824

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-132 <SIM>

A;Cross-references: GB:AE003883; GB:AE003849; NID:99105115; PIDN:AAF83115.1; GSPDB:GN001

A;Experimental source: strain 95c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.; A-

Brienes, M.R.P.; Bueno, M.E.A.; Camargo, L.E.A.; Carrera, D.M.; Carrer, H.

as-Nero, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A;Authors: Ferreira, V.C.A.; Freixo, J.A.; Fraga, J.S.; Franca, S.C.; Frohm

J.D.; Junqueira, M.L.; Kieber, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramitsu, E.E.; Laigh

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,

Martins, E.Y.; Menck, C.P.M.; Miracula, A.Y.; Oliveira, R.C.; Miyazaki, C.Y./

Palmieri, D.P.; Nunes, L.R.; Oliveira, M.A.; Oliveira, R.C.; Palmeira, R.C.; de Oliveira, R.C.; de Oliveira, R.V.; Sawasaki

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; da Silveira

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira

M.; Tsuchako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XFO304

RESULT 8
 BB3400 hypothetical protein PA1952 [imported] - *Pseudomonas aeruginosa* (strain PAO1)

C;Species: *Pseudomonas aeruginosa*

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: BB3400

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br-

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic patho-

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: BB3400

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-250 <STO>

A;Cross-references: GB:AE004622; GB:AE004091; NID:99947948; PIDN:AAG05340.1; GSPDB:GN001

A;Experimental source: strain PAO1

C;Genetics:

A;Gene: PA1952

RESULT 9
 BB3400 LipCD2 protein [imported] - *Streptococcus pneumoniae* (strain TIGR4)

C;Species: *Streptococcus pneumoniae*

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: A95148

R;Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Held

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,

McKinney, T.; Hickey, B.K.; Holt, T.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-266 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75378.1; PID:gi14972757; GSPDB:GN00164; TIGR:SP4

C;Genetic source: strain TIGR4

C;Genetics:

A;Gene: SP1274

RESULT 10
 BB3405 LipCD Protein [imported] - *Streptococcus pneumoniae* (strain R6)

C;Species: *Streptococcus pneumoniae*

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001

C;Accession: G98015

R;Hosking, J.A.; Albom Jr., W.; Burgert, L.; Dehoff, B.S.; E

e, R.; LeBlanc, D.J.; Lee, J.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McMahen, S.; M

Y. P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A;Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-266 <KUR>

A;Cross-references: GB:AE007317; PIDN:AAK9955.1; PID:gi15458781; GSPDB:GN00174

C;Genetic source: strain R6

C;Genetics:

A;Gene: LicD2

RESULT 11
 BB3405 hypothetical protein [imported] - *Sinorhizobium meliloti* (strain 1021) magaplasmid pSymB

C;Species: *Sinorhizobium meliloti*

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: E95936

R;Finan, T.M.; Nealon, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo-

1 CAYWASRGIRPVG 13

Db 166 CSWZALRFVNP 176

A;Reference number: A95842; MUID:21396508; PMID:11481431
 A;Accession: B95936
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: GB:AU591965; PIDN:CAAC49157.1; PID:gi15140642; GSPDB:GN00167
 A;Experimental source: strain 1021, megaplasmid pSymb
 R;Galibert, P.; Finan, T.M.; Long, S.R.; Phuher, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chaix, P.; Cowie, A.; Davis, R.W.; Dreano, L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kalman, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaurie, hebault, P.; Vandebol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: SMB21253
 A;Genome: Plasmid

RESULT 14
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: EMBL:X63150; NID:G452747; PID:CAA44853.1; PID:9452749.
 C;Species: Escherichia coli
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C;Accession: S43878
 R;Lloosa, M.; Bolland, S.; de la Cruz, F.
 J. Mol. Biol. 235, 448-464, 1994
 A;Title: Genetic organization of the conjugal DNA processing region of the IncW plasmid
 A;Reference number: S43877; MUID:94118301; PMID:828974
 A;Accession: S43878
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: EMBL:X63150; NID:G452747; PID:CAA44853.1; PID:9452749.
 C;Species: Escherichia coli
 C;Accession: S43878
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hoiroyd, S.; Rajandream, M.A.; Rogers, R.J.; Rutten, S.; Seeger, K.; Sketton, S.; Squares, S.; Nature 333, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: D70817
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Cross-references: GB:AL022003; PID:gi3261547; PID:CAA17613.1; PID:g326154
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: Rv1716

RESULT 15
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: GB:AAK65372.1; PID:gi1423833; GSPDB:GN00165
 A;Experimental source: strain 1021, megaplasmid pSymA
 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, P.; Barloy-Hubler, F.; Bows ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti* A;Reference number: A95262; MUID:21396509; PMID:11481432
 A;Accession: B95351
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: GB:AE006469; PIDN:AAK65372.1; PID:gi1423833; GSPDB:GN00165
 A;Experimental source: strain 1021, megaplasmid pSymA
 R;Galibert, P.; Finan, T.M.; Long, S.R.; Phuher, A.; Abola, P.; Barloy-Hubler, F.; Bows ; Peila, D.; Chaix, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspie, N.A.; Fisher, R.W.; L.; Hyman, R.W.; Jones, T.
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaurie, hebault, P.; Vandebol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 C;Contents: annotation
 A;Gene: VirB6

RESULT 13
 AC2368
 hypothetical protein ail4499 [imported] - *Nostoc* sp. (strain PC 7120)
 C;Species: *Nostoc* sp. PC 7120
 A;Note: *Nostoc* sp. strain PC 7120 is a synonym of *Anabaena* sp. strain PC 7120
 C;Accession: AC2368
 C;Accession: AC2368
 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Iriuchii , N.; Shimo, S.; Sugimoto, M.; Tabata, S.; Nakazaki, N.; Matsunaga, S.; Takazawa, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-211, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PC 7120
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AC2368

A;Genome: plasmid

Query Match 49.4%; Score 40.5; DB 2; Length 313;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 10; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

Qy 2 AWAS-----RGIRPVGR 14
Db 285 AWASHTVRAAHRGVRAWGR 304

RESULT 16
E70837 Hypothetical protein Rv0295c - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Accession: E70837 Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Peitwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393: 537-544, 1998
A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A.Reference number: A70500; PMID:9634230
A.Accession: E70837
A.Status: preliminary: nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-267 <CDS>
A.Experimental source: strain H37RV
C.Genetics:
C.Superfamily: Mycobacterium tuberculosis hypothetical protein Rv0295c

Query Match 48.8%; Score 40; DB 2; Length 267;
Best Local Similarity 54.5%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPV 12
Db 197 AWFAEEGGIDPI 207

RESULT 17
B75254 acetate kinase - Deinococcus radiodurans (strain R1)

C.Species: Deinococcus radiodurans
C.Accession: B75254 Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A.Reference number: A75250; MUID:20036896; PMID:10567266
A.Accession: B75254
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-398 <WHLI>
A.Cross-references: GB:AB0002089; GB:AE000513; PID:96460427; PID:AAF12139.1; PID:9646042
A.Experimental source: strain R1
C.Genetics:
A.Map position: 1
C.Superfamily: acetate kinase

Query Match 48.8%; Score 40; DB 2; Length 398;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ANYASRGIRPVG 13
Db 161 AWTSQHGVRRYGR 172

RESULT 18
S54589 AEP2 protein - Yeast (Saccharomyces cerevisiae)
C.Species: Saccharomyces cerevisiae
C.Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
R;Accession: S54589; S19045; S14053; S48307; B55096
R;Pearson, D.; Bowman, S.
Submitted to the EMBL Data Library, May 1995
A;Reference number: S54582
A;Accession: S54589
A;Molecule type: DNA
A;Residues: 1-580 <PEA>
A;Cross-references: EMBL:Z49704; PID:9825540; PID:CAA89780.1; PID:9825548; MIPS:YMR282C
A;Experimental source: strain AB372
R;Finnean, P.M.; Payne, M.J.; Keramidaris, B.; Lukins, H.B.
Curr. Genet. 20, 53-61, 1991
A;Title: Characterization of a yeast nuclear gene, AEP2, required for accumulation of miRNA
A;Reference number: S19045; MUID:92035073; PMID:1718609
A;Accession: S19045
A;Molecule type: DNA
A;Residues: 1-337,'W',339-480,'V',482-580 <FIN>
A;Cross-references: EMBL:M5960; PID:971033; PID:AAA34412.1; PID:9171034
R;Ackerman, S.H.; Gatti, D.L.; Gallefors, P.; Douglas, M.G.; Trzagojoff, A.
PEBS Lett. 278, 234-238, 1991
A;Title: Atp13, a nuclear gene of *Saccharomyces cerevisiae* essential for the expression
A;Reference number: S14053; MUID:91122292; PMID:1825065
A;Accession: S14053
A;Molecule type: DNA
A;Residues: 1-213,'N',215-362,'TIVP',367,'YSFQS'
A;Cross-references: EMBL:X56215; PID:93394; PID:CAA39672.2; PID:95679710
R;Astrom, S.U.; Byström, A.S.
A;Description: Riti1, a tRNA backbone modifying enzyme that mediates initiator/elongator
A;Title: Riti1, a tRNA backbone-modifying enzyme that mediates initiator/elongator
A;Reference number: S48306
A;Accession: S48307
A;Molecule type: DNA
A;Residues: 1-108 <AST>
R;Aastrom, S.U.; Byström, A.S.
Cell 79, 535-546, 1994
A;Title: Riti1, a tRNA backbone-modifying enzyme that mediates initiator and elongator tRNA
A;Accession: B55096
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-11,'V',13-108 <ASW>
A;Cross-references: EMBL:X80095; PID:9556674; PID:CAA56771.1; PID:9556676
A;Note: authors translated the codon TGG for residue 2 as Thr, and GAT for residue 80 as
C;Genetics:
A;Gene: SGD:APB2; ATP13
A;Cross-references: SGD:S0004895; MIPS:YMR282C
A;Map position: 13R
A;Genome: nuclear
C;Function:
A;Description: required for the expression of ATP synthase subunit 9
C;Superfamily: Saccharomyces cerevisiae AEP2 protein
C;Keywords: mitochondrion

Query Match 48.8%; Score 40; DB 2; Length 580;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WYASRGIRP 11
Db 439 WYASRKLRP 447

RESULT 19
I64045 recombination protein rec2 - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 25-Aug-2003
C;Accession: F64045
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkinness, E.P.; Kerlavage, A.;Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, N.S.M.
Science 269, 496-512; 1995
A;Authors: Gheim, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
A;Reference number: A640000; MUID:55350530; PMID:7542800
A;Accession: 164045
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-788 <TIGR>
C;Cross-references: GB:U32691; GB:L42023; NID:91573004; PIDN: AAC21739.1; PID:91573009; T
C;Genetics:
C;Superfamily: competence protein ComC
C;Genes: fec2
C;Molecule type: DNA
A;Residues: 1-181 <KUR>
A;Cross-references: GB:BA0000119; PIDN: PAB75695.1; PID:917133131; GSPDB:GN00179
C;Accession: AB2305
C;Species: *Nostoc* sp. PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AB2305
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, N.;Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena*
A;Reference number: AB1807; MUID:21595285; PMID:11753840
A;Accession: AB2305
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-181 <KUR>
A;Cross-references: GB:BA0000119; PIDN: PAB75695.1; PID:917133131; GSPDB:GN00179
C;Accession: AB2305
C;Species: *Nostoc* sp. PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AB2305
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet submitted to the Protein Sequence Database, January 2000
A;Reference number: Z24180
A;Molecule type: DNA
A;Status: preliminary
A;Cross-references: EMBL:AL132959
A;Experimental source: cultivar Columbia; BAC clone P15G16
C;Genetics:
A;Map position: 3
A;Introns: 39/1; 678/2; 698/3; 773/2
A;Note: F15G16.60
RESULT 20
T47939
hypothetical protein F15G16.60 - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47959
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet submitted to the Protein Sequence Database, January 2000
A;Reference number: T47959
A;Molecule type: DNA
A;Status: preliminary
A;Cross-references: EMBL:AL132959
A;Experimental source: cultivar Columbia; BAC clone P15G16
C;Genetics:
A;Map position: 3
A;Introns: 39/1; 678/2; 698/3; 773/2
A;Note: F15G16.60
RESULT 21
T5841
probable membrane protein - *Streptomyces coelicolor*
C;Species: *Streptomyces coelicolor*
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T5841
R;Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A;Reference number: Z21400
A;Accession: T5841
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-184 <HAR>
A;Cross-references: EMBL:AL031260; PIDN:CAA20292.1; GSPDB:GN000670; SCOEDB:SC9A10_05C
C;Accession: SC9A10_05C
Query Match 48 8%; Score 40; DB 2; Length 790;
Best Local Similarity 63.6%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 2;
Qy 4 YASRGIRPVGR 14
Db 373 YGSRGHQPER 383
RESULT 22
T5841
probable acetyltransferase - *Deinococcus radiodurans* (strain R1)
C;Species: *Deinococcus radiodurans*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: F75556
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.;Shen, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A;Reference number: A755250; MUID:20036896; PMID:10557266
A;Accession: F75556
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-171 <WHI>

RESULT 24

H82925 hypothetical protein uvl63 [Imported] - Ureaplasma urealyticum
 C;Species: Ureaplasma urealyticum
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: HB2325
 R;Glass, J.T.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H.
 Submitted to GenBank, February 2000
 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minor
 A;Reference number: A82870
 A;Accession: H82925
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-260 <GLN>
 A;Cross-references: GB:AE002116; GB:AF222894; NID:96899118; PIDN:AAF30569.1; GSPDB:GN001
 A;Experimental source: serovar 3; biovar 1
 C;Genetics:
 A;Gene: UU163
 A;Genetic code: SGCS
 C;Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match Score 47.6%; DB 2; Length 260;
 Best Local Similarity 54.5%; Pred. No. 52; ^{Score 39;}
 Matches 6; Conservative 3; Indels 0; Gaps 0;
 Qy 3 WYASRGRPVG 13
 Db 176 WYASDGVGKIG 186

Query Match Score 47.6%; DB 2; Length 333;
 Best Local Similarity 63.6%; Pred. No. 66; ^{Score 39;}
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 WYASRGRPVG 13
 Db 58 WLGRGDREVG 68

RESULT 25

A87709 formamidopyrimidine-DNA glycosylase CC3707 [Imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C;Accession: A87709
 R;Nierman, W.C.; Felbilyan, T.V.; Paulsen, I.T.; Nelson, K.E.; Heidelberg, J.B.; Laub, M.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; PMID:21173698; PMID:11259647
 A;Accession: A87709
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-315 <SP0>
 A;Cross-references: GB:AE005673; NID:913425473; PIDN:AAF25669.1; GSPDB:GN00148
 C;Genetics:
 A;Gene: CC3707
 C;Superfamily: formamidopyrimidine-DNA glycosidase

Query Match Score 47.6%; DB 2; Length 315;
 Best Local Similarity 50.0%; Pred. No. 62; ^{Score 39;}
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 AWYASRGRPVG 13
 Db 168 AWFAAMGEPEPLG 179

Query Match Score 47.6%; DB 2; Length 374;
 Best Local Similarity 60.0%; Pred. No. 73; ^{Score 39;}
 Matches 9; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
 Qy 3 WYASR---GIRPYG 13
 Db 171 WLGRDRNSNGIRPYG 185

RESULT 26

H82852 hydroxybenzoate octaprenyltransferase Xf0068 [Imported] - Xylella fastidiosa (strain 9as)

C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
 C;Accession: H82852
 R;Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: For a complete list of authors see reference number A59328 below
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-333 <SIM>

B38176 samB protein - Salmonella typhimurium

C;Species: Salmonella typhimurium
 C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 20-Jun-2000
 C;Accession: B38176
 R;Nohmi, T.; Hakura, A.; Nakai, Y.; Murayama, S.Y.; Sofuni, T.
 J; Bacteriol. 173, 1051-1063, 1991
 A;Title: Salmonella typhimurium has two homologous but different umUDC operons: cloning
 A;Reference number: A38176; MUID:91123176; PMID:1991707
 A;Accession: B38176
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-424 <NOH>
 A;Cross-references: GB:D90202; NID:9217087; PIDN:BAAl4226.1; PMID:9217089
 A;Experimental source: strain LT2
 C;Genetics:
 A;Gene: samB
 C;Function:
 A;Description: restores JV mutability; involved in mutagenesis
 C;Keywords: umuc protein
 C;Superfamily: DNA repair; induced mutagenesis; SOS mutagenesis

Query Match 47.6%; Score 39; DB 2; Length 424;
 Best Local Similarity 66.7%; Pred. No. 83;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WYASRGIRP 11
 Db 390 WFAGRGIAA 398

RESULT 29

AB034 UV protection protein [Imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain AB034) C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 A;Note: This species has also been called *Salmonella typhi*
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AB1034 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gara, P.
 Nature 413, 848-852, 2001
 A;Authors: Party, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi - *Salmonella* enterica serovar Typhi (strain AB034) C;Reference number: AB0302; MUID:21534947; PMID:11677608
 A;Accession: AB1034
 A;Molecule type: DNA
 A;Residues: 1-424 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD06719.1; PMID:916505372; GSPDB:GN00176
 A;Genetics:
 A;Gene: samB
 C;Superfamily: umuc protein

Query Match 47.6%; Score 39; DB 2; Length 424;
 Best Local Similarity 66.7%; Pred. No. 83;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WYASRGIRP 11
 Db 390 WFAGRGIAA 398

RESULT 30

JN8EGT 9-Glycerol-3-phosphate transport protein - *Escherichia coli* (strain K-12)
 C;Species: *Escherichia coli* names: Glycerol-3-phosphate permease
 C;Accession: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 01-Mar-2002
 R;Eiglmeier, K.; Boos, W.; Cole, S.T.
 Mol.Microbiol. 1, 251-258, 1987
 A;Title: Nucleotide sequence and transcriptional startpoint of the glpt gene of *Escherichia coli*-3-phosphate permease system
 A;Reference number: S00868; MUID:3323281; PMID:88201663;
 A;Molecule type: DNA
 A;Accession: S00868
 A;Residues: 1-452 <EIG>
 A;Cross-references: EMBL:Y00536; NID:941586; PIDN:CAA68598.1; PMID:941587
 A;Experimental source: strain K12
 R;Blattner, F.R.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, R.; Perera, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, R.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamitis, K.; Apodaca, L.; Title: Genome sequence of *enterohemorrhagic Escherichia coli* O157:H7
 A;Reference number: A85480; MUID:21074935; PMID:11205551
 A;Accession: G55863
 A;Status: preliminary

A; Molecule type: DNA
A; Residues: 1-452 <STO>
A; Cross-references: GB:AE005174; NID:912516580; PIDN:AGG57371.1; GSPDB:GN00145; UNGP:2334
A; Experimental source: Strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: GlpT
C; Superfamily: hexose phosphate transport protein unpt

Query Match 47.6%; Score 39; DB 2; Length 452;
Best Local Similarity 42.9%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CAYWASRGIRGVGR 14
Db 130 CGMFQGMWPPCCR 143

RESULT 33

T43558 sulfide dehydrogenase (coenzyme Q2) (EC 1.8.5.-) precursor, mitochondrial [validated] -
Species: Schizosaccharomyces pombe
C; Sequence revision 21-Jan-2000 #text_change 21-Jul-2000
C; Date: 21-Sep-2000 #sequence_revision 21-Sep-1990 #text_change 08-Oct-1999
C; Accession: T43558; T40163
R; Vandae Wiegse, J.G.; Ow, D.W.
J; Biol. Chem. 274: 13250-13257, 1999
A; Title: A fission yeast gene for mitochondrial sulfide oxidation.
A; Reference number: Z22577; MUID:99240711; PMID:10224084
A; Accession: T43558
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-459 <VAN>
A; Cross-references: EMBL:AF042283; NID:95256827; PIDN:ADD41159.1; PID:95256828
R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lejaune, V.; Galibert, F.
Submitted to the EMBL Data Library, October 1998
A; Reference number: Z21908
A; Accession: T40163
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-459 <WOO>
A; Cross-references: EMBL:AU03395; PIDN:CAA21882.1; GSPDB:GN00067; SPDB:SPBC2G5_06c
A; Experimental source: strain 972h-; cosmid c2G5
C; Genetics:
A; Gene: hmt2; SPBC2G5_06c
A; Map position: 2
C; Function:
A; Description: catalyzes the reduction of quinone (coenzyme Q2) by sulfide [validated]. M
A; Note: proposed to function as a sulfide quinone oxidoreductase
C; Keywords: mitochondrial; oxidoreductase
P; 1-24/Domain: transit peptide (mitochondrion) #status Predicted <TNP>
P; 23-459/Product: sulfide dehydrogenase, mitochondrial #status predicted <MAT>

Query Match 47.6%; Score 39; DB 2; Length 459;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WYASRGIRPV 11
Db 445 WYGSGGLIP 453

RESULT 34

D84258 alcohol dehydrogenase [imported] - Halobacterium sp. NRC-1
Species: Halobacterium sp. NRC-1
C; Sequence revision 02-Feb-2001 #text_change 02-Feb-2001
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
R; Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danon, M.J.; Hough, D.W.; Maddocks, D.G.; Jacobson, T.; Jung, P.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebbhardt, H.; Lowe, T.M.; Li
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950

Query Match 47.6%; Score 39; DB 2; Length 600;
Best Local Similarity 45.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPV 12
Db 552 AWHCIRGVVPI 562

RESULT 35

A35548 319K protein ndvB - Rhizobium meliloti
Species: Rhizobium meliloti
C; Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 08-Oct-1999
C; Accession: A35548
R; Ielpi, L.; Dylan, T.; Ditta, G.S.; Helinski, D.R.; Stanfield, S.W.
J. Biol. Chem. 265: 2843-2851, 1990
A; Title: The ndvB locus of Rhizobium meliloti encodes a 319-kDa protein involved in the
A; Reference number: A35548; MUID:90153914; PMID:2154461
A; Accession: A35548
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-2870 <IEL>
A; Cross-references: GB:U05219; NID:9152270; PIDN:AAA26305.1; PID:9152271
C; Keywords: transmembrane protein

Query Match 47.6%; Score 39; DB 2; Length 2870;
Best Local Similarity 50.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WYASRGIRPV 12
Db 1126 WYRTIGLEPM 11356

RESULT 36

H72507 83-101, 1999
hypothetical protein APE2038 - Aeropyrum pernix (strain K1)
Species: Aeropyrum pernix
C; Sequence revision 20-Aug-1999 #text_change 09-Jun-2000
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
R; Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Funahashi, T.; Tanaka, T.; Kawa, H.; Takamiya, M.; Masuda, S.; DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyperthermophilic Crenarchaeon, Aeropyrum pernix K1
A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Accession: H72507
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-121 <KAW>
A; Cross-references: DDBJ:AP000063; NID:95105654; PIDN:BAAB1048.1; PID:di1044834; PID:95105654
A; Experimental source: strain K1
C; Superfamily: Aeropyrum pernix hypothetical protein APE2038
A; Gene: APE2038
C; Genetics:

Query Match 46.3%; Score 38; DB 2; Length 121;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAYWASRGIRPVGR 14
Db 43 CGYARSSIRTPAR 56

RESULT 37
DB7357 hypothetical protein C0871 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: D87357
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Emiolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11253647
A;Accession: D87357
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-194 <STO>
A;Cross-references: GB:AB005673; NID:913422132; PIDN:AAK22856.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0871

RESULT 40
SC8784 cathepsin L - Paramecium tetraurelia (fragment)
C;Species: Paramecium tetraurelia
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 03-Nov-2000
C;Accession: S68784
R;Voeikel, H.; Kurz, U.; Lindner, J.; Klumpp, S.; Gnau, V.; Jung, G.; Schultz, J.E.
Eur. J. Biochem. 238, 198-206, 1996
A;Title: Cathepsin L is an intracellular and extracellular protease in Paramecium tetrau
A;Reference number: S68783; MUID:96248439; PMID:8665938
A;Accession: S68784
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-294 <STO>
A;Cross-references: EMBL:X91756; NID:91403088; PID:91403089
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1995
C;Genetics:
A;Gene: SC8784

RESULT 46
H72646 hypothetical protein AP00606 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Accession: H72646
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takami, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Accession: H72450; MUID:99310339; PMID:10382966
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-338 <KAW>
A;Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BA079576.1; PID:9510
A;Experimental source: strain K1
C;Genetics:
A;Gene: AP00606

Query Match 46.3%; Score 38; DB 2; Length 238;
Best Local Similarity 63.6%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 126 AWYASRGIRPV 12
Db 126 AWYASRGIRPV 136

Search completed: February 25, 2004, 06:44:24
Job time : 21 secs

RESULT 39
F95120 hydrolase, probable [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Accession: F95120
R;Tettelein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
Science, 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, P.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Accession: F95120
A;Status: preliminary

Scoring table:	BLOSUM62	RESULT 1
Gapop:	10.0 , Gapext 0.5	PRRP_HUMAN STANDARD; PRT; 87 AA.
Searched:	141681 seqs., 52070155 residues	ID PRRP_HUMAN AC P8177; DT 30-MAY-2000 (Rel. 39, Created) DT 30-MAY-2000 (Rel. 39, Last sequence update)
Total number of hits satisfying chosen parameters:	141681	DB 28-FEB-2003 (Rel. 41, Last annotation update)
Minimum DB seq length: 0		DE Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP20].
Maximum DB seq length: 2000000000		DE DE PRRP31
Post-processing: Minimum Match 0%		DE DE PRRP20
Post-processing: Maximum Match 100%		GN Homo sapiens (Human)
Database :	SwissProt_42::*	OS Homo sapiens (Human);
Scoring table:	BLOSUM62	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sequence:	1 CAVYASRGIRPVGRX 15	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Scoring table:	BLOSUM62	NCBI_TaxID=9606;
Gapop:	10.0 , Gapext 0.5	RN [1] -
Searched:	141681 seqs., 52070155 residues	RP RP SEQUENCE FROM N.A.
Total number of hits satisfying chosen parameters:	141681	RP TISSUE=Brain; RC
Minimum DB seq length: 0		RX MEDLINE=96268781; PubMed=9607765;
Maximum DB seq length: 2000000000		RA Hiruma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
Post-processing: Minimum Match 0%		RA Kitada C., Maeda Y., Asano T., Matsunoto H., Sekiguchi M.,
Post-processing: Maximum Match 100%		RA Kurokawa T., Nishimura O., Onda H., Fujino M.,
Database :	SwissProt_42::*	RA RT "A prolactin-releasing Peptide in the brain.";
Scoring table:	BLOSUM62	RL Nature 393:272-276(1998).
Sequence:	1 CAVYASRGIRPVGRX 15	RN [2] -
Scoring table:	BLOSUM62	RP TISSUE SPECIFICITY.
Gapop:	10.0 , Gapext 0.5	RX MEDLINE=99426552; PubMed=10498338;
Searched:	141681 seqs., 52070155 residues	RA Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hiruma S.,
Total number of hits satisfying chosen parameters:	141681	RA Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
Minimum DB seq length: 0		PA Sumio Y., Fujino M.,
Maximum DB seq length: 2000000000		RT RT Tissue distribution of prolactin-releasing peptide (PrRP) and its receptor.;
Post-processing: Minimum Match 0%		RL Regul. Pept. 83:1-10(1999).
Post-processing: Maximum Match 100%		CC -!- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.
Database :	SwissProt_42::*	CC -!- TISSUE SPECIFICITY: Medulla oblongata and hypothalamus.
Scoring table:	BLOSUM62	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sb-sib.ch).
Sequence:	1 CAVYASRGIRPVGRX 15	CC EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		FT MOD RES 53 53 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	SQ SEQUENCE 87 AA; 9639
Scoring table:	BLOSUM62	EMBL: AB015419; BAA29027.1; -
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
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Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum DB seq length: 0		FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRRP20.
Maximum DB seq length: 2000000000		FT PEPTIDE 34 53 PROTEIN amidation.
Post-processing: Minimum Match 0%		FT PROPEP 58 53 AMIDATION (G-54 PROVIDE AMIDE GROUP).
Post-processing: Maximum Match 100%		SQ SEQUENCE 87 AA; 9639 MW; 229AZF3P5OCF9B1B CRC64;
Database :	SwissProt_42::*	EMBL: AB015419; BAA29027.1; -
Scoring table:	BLOSUM62	DR DR MIM: 602663; F:peptide hormone: TAS.
Gapop:	10.0 , Gapext 0.5	DR GO: GO:0005180; Hormone; Amidation; Signal.
Searched:	141681 seqs., 52070155 residues	KW KW BY SIMILARITY.
Total number of hits satisfying chosen parameters:	141681	FT SIGNAL 1 22 PROLACTIN-RELEASING PEPTIDE PRRP31.
Minimum		

Query	Match	Score 72;	DB 1;	Length 87;		
Best Local Similarity	100.0%	Pred. No. 8.8e-06;				
Matches	13;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	2 AWYASRGKRPVGR 14					
Db	40 AWYASRGKRPVGR 52					
RESULT 2						
PRRP_BOVIN	STANDARD;	PRT;	98 AA.			
P8264; PRP_BOVIN						
AC						
30-MAY-2000 (Rel. 39, Created)						
30-MAY-2000 (Rel. 39, Last sequence update)						
DT						
28-FEB-2003 (Rel. 41, Last annotation update)						
DE						
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP20].						
PRH.						
Bos taurus (Bovine).						
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bosidae; Bovinae; Bos.						
NCBI_TaxID=913;						
OX						
SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.						
PRRP						
TESSUE=BRAIN; STANDARD;						
MEDLINE=98266781; PubMed=9607765;						
Hiruma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Matsuo Y., Asano T., Kurokawa T., Nishimura O., Onda H., Kurokawa T., Nishimura O., Onda H., Fujino M.; "A prolactin-releasing peptide in the brain."; Nature 393:272-276(1998).						
-1- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.						
-1- TISSUE SPECIFICITY: Medulla oblongata and hypothalamus.						
CC						
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CC						
EMBL; AB01517; BAA29025.1; -						
KW Hormone; Amidation; Signal; Cleavage on pair of basic residues.						
SIGNAL	22					
PEPTIDE	23	53				
PEPTIDE	33	53				
PROPEP	58	98				
MOD RES	53	1054 MW;	AMIDATION (G-54 PROVIDE AMIDE GROUP).			
SEQUENCE	98 AA;	08AC35A13-B0FA908 CRC64;				
SQ						
Query	Match	Score 68;	DB 1;	Length 98;		
Best Local Similarity	92.3%	Pred. No. 5e-05;				
Matches	12;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
Dy	2 ANYASRGKRPVGR 14					
Db	40 ANYASRGKRPVGR 52					
RESULT 3						
PRRP_RAT	STANDARD;	PRT;	83 AA.			
AC	P81278; Q8K3Y0;					
DT	30-MAY-2000 (Rel. 39, Created)					
DT	30-MAY-2000 (Rel. 39, Last sequence update)					
DT	28-FEB-2003 (Rel. 41, Last annotation update)					
OS Rattus norvegicus (Rat)						
OC Bokayote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.						
NCBI_TaxID=10116;						
RN [1]						
RP SEQUENCE FROM N.A. (ISOFORM 1).						
RC TISSUE=Brain;						
RX MEDLINE=98266781; PubMed=9607765;						
RA Hiruma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Matsuo Y., Asano T., Kurokawa T., Nishimura O., Onda H., Kurokawa T., Nishimura O., Onda H., Fujino M.; "Quantitation of Prolactin-releasing peptide (PrRP) mRNA expression in specific brain regions during the rat oestrous cycle and in lactation.";						
RN [2]						
RP SEQUENCE FROM N.A. (ISOFORM 2).						
STRAIN=Sprague-Dawley; TISSUE=Hypothalamus;						
RA Anderson S.T., Kobay I.C., Lang T., Grattan D.B., Curlewis J.D.; "Quantitation of Prolactin-releasing peptide (PrRP) mRNA expression in the rat oestrous cycle and in lactation.";						
RN [3]						
RP TISSUE SPECIFICITY.						
RX MEDLINE=99426652; PubMed=10498338;						
RA Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hiruma S., Fujino M.; "Tissue distribution of prolactin-releasing peptide (PrRP) and its receptor"; RT Regul. Pept. 83:1-10(1999).						
RA Sumano Y., Fujino M.; "FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL. CC -! ALTERNATIVE PRODUCTS: CC -! TISSUE SPECIFICITY: Widely expressed, with highest levels in medulla oblongata and hypothalamus.						
CC Name=1; IsoId=P81278-1; Sequence=Displayed;						
CC Name=2; IsoId=P81278-2; Sequence=ISP004370; Sequence=ISP004370;						
CC -! TISSUE SPECIFICITY: Widely expressed, with highest levels in medulla oblongata and hypothalamus.						
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CC						
CC EMBL; AB015418; BAA29026.1; -						
CC DR EMBL; AF521910; BAA82154.1; -						
CC DR PIR; JC7607; JC7607.						
CC KW Hormone; Amidation; Signal; Cleavage on pair of basic residues.						
CC FT SIGNAL	1					
FT PEPTIDE	22	52				
FT PEPTIDE	33	52				
FT PROTEP	57	83				
FT MOD RES	52	52				
FT VARSPIC	33	83				
FT DRGTTKFSORG -> SECITYGQPLTSFHFFTSQMP (Isoform 2)						
FT FT ID=VSP_004370. Doc75A264EEB4F29 CRC64;						
FT SQ SEQUENCE 83 AA; 9215 MW;						
Query Match Score 64;	DB 1;	Length 83;				
Best Local Similarity 84.6%;						
Matches 11; Conservative 0;	Mismatches 2;	Indels 0;				
FT Matches 11; Conservative 0;	Mismatches 2;	Indels 0;				
FT G						
FT TPDINPAWYTGGIRPVGRGRRATPRDVIGLQQLSCLPL						
FT DRGTTKFSORG -> SECITYGQPLTSFHFFTSQMP (Isoform 2)						
FT FT ID=VSP_004370. Doc75A264EEB4F29 CRC64;						

Qy	2 AWYASRGIRPVGR 14	Db	39 AWYTGRCGIRPVGR 51	
RESULT 4				
NRPI_YEAST	STANDARD;	PRT;	719 AA.	
ID_NRPI YEAST				
AC_P32770; Q12228;				
DT_01-OCT-1993 (Rel. 27, Created)				
DT_01-NOV-1997 (Rel. 35, Last sequence update)				
DT_28-FEB-2003 (Rel. 41, Last annotation update)				
DE_Asparagine-rich Protein (ARP protein).				
DE_NRPI OR ARP1 OR ARP OR YDL167C.				
OS_Saccharomyces cerevisiae (Baker's yeast).				
OC_Eukaryota; Fungi; Ascomycota; Saccharomycetes;				
OC_Saccharomycetales; Saccharomycetaceae; Saccharomyces.				
NCBI_TaxID=4932;				
RN [1]				
RP_SEQUENCE FROM N.A.				
RC_STRAIN=AH22;				
EX_MEDLINE=932477548; PubMed=8483449;				
RA_Wehner E.P.; Rao P.; Brendel M.;				
RT_Molecular structure and genetic regulation of SFA, a gene				
RT_responsible for resistance to formaldehyde in <i>Saccharomyces</i>				
RT_cerevisiae, and characterization of its protein product.;"				
RL_Mol. Genet. 237:351-358 (1993).				
RN [2]				
RP_SEQUENCE FROM N.A.				
RC_STRAIN=ES288C;				
RA_Pohl T.M.;				
RL_Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.				
CC_- SIMILARITY: Contains 2 RANBP2-type zinc fingers.				
CC_- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.				
CC_				
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CC or send an email to license@isb-sib.ch).				
CC_				
DR_EMBL; X68020; CAA48159.1; -.				
DR_EMBL; Z67750; CA991579.1; -.				
DR_EMBL; Z74215; CA998741.1; -.				
DR_PIR; S61046; S61046.				
DR_GerOnline; 140410.				
DR_SGD; SGD002326; NRP1.				
DR_InterPro; IPR000504; RNA_rec_mot.				
DR_InterPro; IPR001676; Znf_RanGDP.				
DR_Pfam; PF00076; zrm; 1.				
DR_Pfam; PF00641; zf-RanBP; 2.				
DR_SMART; SM00360; RRM; 1.				
DR_SMART; SM00547; znf_RBZ; 2.				
DR_Positive; PS55102; RRM; 1.				
DR_Positive; PS50030; RRM; RNP_1; FALSE_NEG.				
DR_Positive; PS01358; ZFP_RANBP2; 2.				
DR_Positive; PS50199; ZFP_RANBP2; 2.				
KW_Nuclear Protein; Zinc_finger; RNA-binding; Repeat.				
FT_DOMAIN 226	322			
FT_ZN_FING 355	384			
FT_ZN_FING 581	610			
FT_DOMAIN 490	564			
FT_DOMAIN 493	493			
FT_CONFLICT 493	493			
SEQ_SEQUENCE 719 AA;	79299 MW;	ADA9BC09FD582669 CRC64;		
Query Match	53.7%	Score 44; DB 1; Length 719;		
Best Local Similarity	50.0%	Prd. No. 5.6;		
Matches	6;	Conservative		
	3;	Mismatches	3;	
		Indels	0;	
		Gaps	0;	

Query Match 50.0%; Score 41; DB 1; Length 402;
 Best Local Similarity 47.4%; Pred. No. 11;
 Matches 9; Conservative 1; Mismatches 1; Indels 8; Gaps 1;

Qy 3 WYASRG-----IRPGV 13
 Sq 91 WYAPRQLSLRAETKPGV 109

RESULT 7
 RECJ_ERWCH
 ID RECJ_ERWCH STANDARD PRT; 575 AA.
 AC P39633; Q41007;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-).
 GN RECJ
 OS Erwinia chrysanthemi
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lovett S.T.; Tzomeva M.; Sutera V.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases
 RN [2]
 RP SEQUENCE OF 1-100 FROM N.A.
 RC STRAN=3937;
 RX MBIDLINE=91222048; PubMed=8168497;
 RB Sherchik V.B.; Condeine G.; Robert-Baudouy J.;
 RT "Characterization of DsbC, a periplasmic protein of Erwinia
 chrysanthemi and Escherichia coli with disulfide isomerase
 activity";
 RL EMBO J. 13:2007-2012 (1994).

-!- CC SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASB. REQUIRED FOR
 MANY TYPES OF RECOMBINATIONAL EVENTS, ALTHOUGH THE STRINGENCY OF
 THE REQUIREMENT FOR RECJ APPEARS TO VARY WITH THE TYPE OF
 RECOMBINATIONAL EVENT MONITORED AND THE OTHER RECOMBINATION GENE
 PRODUCTS WHICH ARE AVAILABLE (BY SIMILARITY).
 CC

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 or send an email to license@isb-sib.ch).

CC DR U57963; AAB02611; -;
 CC EMBL:X76587; CAA54109; -;
 CC InterPro; IPR03156; DHEA1.
 CC InterPro; IPR01667; Pposterase.
 CC DR InterPro; IPR04610; RecJ.
 CC DR Pfam; PF01368; DHH; 1.
 CC DR PTam; PF0272; DHHA1; 1.
 CC DR TIGRFAMS; TIGR0644; recJ; 1.
 CC KW Hydrolase; Nuclease; Exonuclease.
 CC FT MNVVTQ -> MLPPN (IN REF. 2).
 CC FT CONFLICT 1 6 R -> G (IN REF. 2).
 CC FT CONFLICT 83 83 R -> H (IN REF. 2).
 CC FT CONFLICT 100 100 R -> H (IN REF. 2).
 CC SQ SEQUENCE 575 AA; 4D06A037DFD3DBE4 CRCC4;

Query Match 48.8%; Score 40; DB 1; Length 575;
 Best Local Similarity 55.6%; Pred. No. 23;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAWYARGI 9
 Sq 1 CAWYARGI 9
 DB 208 CGWFÆRGVL 216

DR EMBL; AE939122; CA05901; 1.
 DR HAMAP; MF_00378; 1.
 DR InterPro; IPR010375; 1.
 DR InterPro; IPR004365; tRNA_antI.
 DR Pfam; PF02601; Exonuc_VII_L.
 DR Pfam; PF01336; tRNA_antI; 1.
 DR TIGRFAMS; TIGR0023; xeaA; 1.
 KW Hydrolase; Nuclease; Exonuclease; Complete proteome.
 SEQUENCE 402 AA; 438882 MW;

SQ 14592938372B4E08 CRCE4;

RESULT 8
 ATPU_BEST STANDARD; PRT; 580 AA.
 ID YEAST
 AC P22136; P21115;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-MAR-2004 (Rel. 43, Last sequence update)
 DE ATP13 Protein, mitochondrial precursor.
 DE Eukaryota; Fungi; Ascomycota; Saccharomycetes;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID:4932;
 RN PRT; 580 AA.
 RQ SEQUENCE FROM N.A.; PubMed=1825065;
 RA Ackerman S.H., Gatti D.L., Gellefors P., Douglas M.G., Tzagoloff A.;
 RT "ATP13, a nuclear gene of Saccharomyces cerevisiae essential for the expression of subunit 9 of the mitochondrial ATPase.";
 RT FEBS Lett. 278:234-238(1991).
 RN PRT; 580 AA.
 RQ SEQUENCE FROM N.A.; PubMed=9203507; PubMed=1718609;
 RA Payne M.J., Finnegan P.M., Keramidaris E., Lukins H.B.;
 RT "Characterization of a yeast nuclear gene, ABP2, required for accumulation of mitochondrial mRNA encoding subunit 9 of the ATP synthase.";
 RT Curr. Genet. 20:53-61 (1991).
 RN PRT; 580 AA.
 RC STRAINS=S288C / AB972;
 RX MEDLINE=9713268; PubMed=9169872;
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devin K., Gentle S., Hamlin N., Hunt S., Jagels K., Lye G., Moller S., Odell C., Pearson D., Rajandream M.A., Rice P., Shelton J., Walsh S., Whitehead S., Barrell B.G.;
 RT XIII.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII." Nature 387:90-93 (1997).
 RN PRT; 580 AA.
 RC STRAINS=S288C / YPH1; MEDLINE=95042750; PubMed=7954819;
 RA Aststrom S.U., Bystryöm A.S.;
 RT "Rit1, a tRNA backbone-modifying enzyme that mediates initiator and elongator tRNA discrimination.", Cell 79:535-546 (1994).
 DR PRT; 580 AA.
 CC -!- FUNCTION: Essential for the expression of subunit 9 of the mitochondrial ATPase.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- MISCELLANEOUS: Mutations in ATP13 result in respiratory deficiency.
 CC -!- CAUTION: Ref.1 sequence differs from that shown from position 363 onward and is shorter (372 AA) due to a frameshift.

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CC DR EMBL; X56215; CAA39672.2; ALT_FRAME.
 DR EMBL; X59860; AAC34412.1; -.
 DR EMBL; X49704; CAB89780.1; -.
 DR PIR; S80795; CA956771.1; -.
 DR GerOnLine; 142987; -.
 DR SGD; S0004895; ABP2.
 KW TRANSIT 1 25 MITOCHONDRION (OR 28) (POTENTIAL).
 FT CHAIN 26 580 ATPI3 PROTEIN.

FT CONFLICT 214 214 G -> N (IN REF. 1).
 FT CONFLICT 481 481 I -> V (IN REF. 1).
 SQ SEQUENCE 580 AA; BC0A10EABCDAA CRC64;

Query Match 48.8%; Score 40; DB 1; Length 580;
 Best Local Similarity 66.7%; Prd. No. 23;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WYARGIRP 11
 Db 439 WYASKRLRP 447

RESULT 9
 REC2_HAETN STANDARD; PRT; 788 AA.
 ID REC2_HAETN AC P4408;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Recombination protein 2.
 GN REC2 OR REC-2 OR HI0061.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BC200;
 RX MEDLINE=94341577; PubMed=8063112;
 RA Clifton S.W., McCarthy D., Roe B.A.;
 RT "Sequence of the rec-2 locus of Haemophilus influenzae: homologies to comc-ORF3 of *Bacillus subtilis* and msba of *Escherichia coli*."
 RL Gene 146:95-100(1994).
 RN PRT; 788 AA.
 RC STRAIN=RQ / KM20 / ATCC 51907;
 RX MEDLINE=953506330; PubMed=7542800;
 RA Fleschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerinney K., Sutton G., Bult J.-F., Dougherty B.A., Merrick J.M., Keravage A.R., Bult C.J., Tomb J.-F., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.O., Spriggs T., Heidelberg J., Brandon R.C., Utterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M., Gneim C.I., McDonald L.A., Small R.V., Fraser C.M., Smith H.O., Venter J.C.;
 RT "Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.", Science 269:496-512(1995).
 CC -!- FUNCTION: Might contribute to transformation as a member of a membrane-bound pore complex at the base of the transformosome. It could directly interact with transforming DNA during translocation - indirectly by participating in the assembly of the pore.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (Potential).
 CC -!- SIMILARITY: TO B.SUBTILIS COMEC, N.GONCRHOAE COMA, AND E.COLI YCAI.

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CC DR EMBL; L20805; AAC13733.1; -.
 DR EMBL; U32691; AAC21739.1; -.
 DR PIR; 164045; 164045.
 DR TIGR; HI0061;
 DR InterPro; IPR01279; Blactmase-like.
 DR InterPro; IPR004477; ComEC_N-term.

DR InterPro; IPR004797; ComEC_Fec2.
 DR Pfam; PF03772; Competence; 1.
 DR Pfam; PF00753; lactamase_B; 1.
 DR TIGRFAMS; TIGR00360; ComEC_Nterm; 1.
 DR TIGRFAMS; TIGR00361; ComEC_Rec2; 1.
 DR TIGRFAMS; TIGR00361; ComEC_Rec2; 1.
 KW Competence; Transport; Inner membrane; Transmembrane;
 KW Complete proteome;
 FT TRANSMEM 3 23
 FT TRANSMEM 27 47
 FT TRANSMEM 51 71
 FT TRANSMEM 226 246
 FT TRANSMEM 263 283
 FT TRANSMEM 313 333
 FT TRANSMEM 367 387
 FT TRANSMEM 401 421
 FT TRANSMEM 434 454
 FT TRANSMEM 456 476
 FT TRANSMEM 508 528
 FT TRANSMEM 748 788
 FT CONFLICT 748
 SQ SEQUENCE 788 AA; 89355 MW; F31104595CB4E47A CRC44;
 QY 3 WYASRGIRPVG 13
 Db 156 WYFSKGITAVG 166

Query Match 48.8%; Score 40; DB 1; Length 788;
 Best Local Similarity 63.6%; Pred. No. 31; Mismatches 3; Indels 0; Gaps 0;

RESULT 11
 EX7L_COREF
 ID EX7L_COREF
 AC Q8FBP1;
 DT 10-Oct-2003 (Rel. 42, Created)
 DT 10-Oct-2003 (Rel. 42, Last sequence update)
 ID PPG_CAUCR
 AC Q9A259;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Formamidopyrimidine-DNA Glycosylase (EC 3.2.2.23) (Fapy-DNA
 Glycosylase)
 DE MUTM OR PFG OR CC3707.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=ATCC 19089 / CB15;
 MEDLINE=11259647; PubMed=11259647;
 RA Nielsen W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newkin A., Stephen C., Phadke N.D., Ely B.,
 RA DeBoe R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Yamaneva J., White O.,
 RA Salberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc. Natl. Acad. Sci. U.S.A.; 98:4136-4141(2001).
 CC -!- FUNCTION: This enzyme may play a significant role in processes
 leading to recovery from mutagenesis and/or cell death by
 alkylating agents (By similarity).
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of DNA containing ring-opened N(7)-
 methylguanine residues, releasing 2,6-diamino-4-hydroxy-5-(N-
 methyl)formamidopyrimidine.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SIMILARITY: Belongs to the FPG family.

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 CC or send an email to license@isb-sib.ch).
 CC EMBL; AE006028; AAK25669; 1; ALT_INIT.
 DR HSSP; O5006; 1; EE8.
 DR TIGR; CC3707;
 DR HAMAP; MF_00103; -1.
 DR InterPro; IPR000191; Fapy_DNA_glyco.
 DR InterPro; IPR00214; Fapy_DNA_Zn_BS.
 DR Pfam; PF01149; Fapy_DNA_glyco; 1.
 DR Prodrom; PD00360; Fapy_DNA_glyco; 1.
 DR TIGRFAMS; TIGR00577; Fpg; 1.
 DR PROSITE; PS01242; FPG; FALSE NEG.
 DR DNA repair; Hydrolase; Glycosidase; Zinc; Zinc-finger;
 KW Complete proteome.
 KW Complete proteome.
 FT ZNFING 260 285
 SQ SEQUENCE 287 AA; 31555 MW; 2D24E20; DC0B5240 CRC64;
 Query Match 47.6%; Score 39; DB 1; Length 287;
 Best Local Similarity 50.0%; Pred. No. 17; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVG 13
 Db 140 AWYASRGIRPVG 151

SEQUENCE FROM N.A.
 RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
 RC MEDLINE=22723752; PubMed=128420036;
 RA Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
 RA Sugimoto S., Matsui K., Yamagishi A., Rikuchi H., Ikeo K.,
 RA Gojobori T.;
 RA RT "Comparative complete genome sequence analysis of the amino acid
 RT replacements responsible for the thermostability of Corynebacterium
 RT efficiens";
 RL Genome Res. 13:1572-1579(2003).
 CC -!- FUNCTION: Bidirectional degrades single-stranded DNA into large
 CC acid-insoluble oligonucleotides, which are then degraded further
 CC into small acid-soluble oligonucleotides (By similarity).
 CC -!- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5' to 3'-
 CC or 3' - to 5' - direction to yield nucleic acid 5'-phosphates.
 CC -!- SUBUNIT: Heterooligomer composed of large and small subunits (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the xsfA family.

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 CC or send an email to license@isb-sib.ch).
 CC EMBL; AP005217; BAC17888; 1; ALT_INIT.
 DR HAMAP; MF_00378; -1.
 DR InterPro; IPR003753; Exonuc_VII_L.

DR InterPro; IPR008994; Nucleic_acid_OB.
DR Pfam; PF02601; Exonuc VII_L; 1.
DR TIGRFAMS; TIGR00237; xsea; 1.
KW Hydrolase; Nuclease; Exonuclease; Complete proteome;
SEQUENCE 413 AA; 45171 MW; D3BABD9687C6EE5D CRC64;

Query Match 47.6%; Score 39; DB 1; Length 413;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 10; Conservative 1; Mismatches 1; Indels 8; Gaps 1;
Qy 2 AWYASRG-----IRPVG 13
Db 91 AFYAGRGSFSLWYTDIYVG 110

RESULT 12
EX7L_CORGL STANDARD; PRT; 417 AA.
ID _BX7L_CORGL
AC QBNRM3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
DB (Exonuclease VII large subunit).
GN XSEA OR CGU1025.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Bidirectionally degrades single-stranded DNA into large
acid-insoluble oligonucleotides, which are then degraded further
into small acid-soluble oligonucleotides (By similarity).
CC -!- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
CC -!- SUBUNIT: Heterooligomer composed of large and small subunits (By
similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the xsea family.

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DR EMBL; AP00527; BAB98418_1; -.
DR HAMAP; MF_00378; -; 1.
DR InterPro; IPR003753; Exonuc VII_L.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR Pfam; PF02601; Exonuc VII_L; 1.
DR TIGRFAMS; TIGR00237; xsea; 1.
KW Hydrolase; Nuclease; Exonuclease; Complete proteome;
SEQUENCE 417 AA; 45582 MW; B32CD286C173C34 CRC64;

Query Match 47.6%; Score 39; DB 1; Length 417;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 10; Conservative 1; Mismatches 1; Indels 8; Gaps 1;
Qy 2 AWYASRG-----IRPVG 13
Db 95 AFYAGRGSFSLWYTDIYVG 114

RESULT 13
SAMR_SALTY STANDARD; PRT; 424 AA.
ID P28322;
AC 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE SanB protein.
GN SAMB.
OS Salmonella typhimurium.
OG Plasmid 60-mba cryptic.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN SEQUENCE FROM N.A.
RC STRAIN=JT2;
RA Nohmi T.; Hakura A.; Nakai Y.; Watanabe M.; Murayama S.Y.;
RA Soroni T.;
RT "Salmonella typhimurium has two homologous but different umuDC
operons: cloning of a new umuDC operon (samAB) present in a
6C-megaditon cryptic plasmid of S. typhimurium.";
RT J. Bacteriol. 173:1051-1063 (1991).
CC -!- FUNCTION: Involved in UV protection and mutation
CC -!- SIMILARITY: Belongs to the DNA polymerase type-Y family.
CC -!- SIMILARITY: Contains 1 umuC domain.
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC DR EMBL; D00202; BAA14226_1; -.
CC DR PIR; B38176; B38176.
CC DR HAMAP; MF_01113; atypical; 1.
CC DR InterPro; IP0001126; UMUC_like.
CC DR Pfam; PF00817; IMS; 1.
CC DR PROSITE; PS50173; UMOC; 1.
CC DR Plasmid; SOS mutagenesis; DNA repair.
CC KW DOMAIN 2 189 UMUC
FT DOMAIN 2 189 UMUC
SQ SEQUENCE 424 AA; FF8C476CC58A2B CRC64;

Query Match 47.6%; Score 39; DB 1; Length 424;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WYASRGIRP 11
Db 390 WFASRGGIAP 398

RESULT 14
GLPT_ECOLI STANDARD; PRT; 452 AA.
ID GLPT_ECOLI
AC P08154;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glyceral-3-phosphate transporter (G-3-P transporter) (G-3-P
permease).
GN GLPT OR B2240.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Eigleman K.; Boos W.; Cole S.;
RT "Nucleotide sequence and transcriptional startpoint of the glpt gene

RT of *Escherichia coli*: extensive sequence homology of the glycerol-3-phosphate transport protein with components of the hexose-6-phosphate transport system.ⁿ
 RT Mol. Microbiol. 1:251-258 (1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 STRAIN=K12; MEDLINE#=74266117; PubMed=9278503;
 RX Blattner F.R.; Plunkett G. III; Bloch C.A.; Perna N.T.; Burland V.;
 RA Itoh T.; Kimura S.; Kitagawa M.; Makino K.; Miki T.; Mitsuhashi N.;
 RA Mizobuchi K.; Mori H.; Nakade S.; Nakamoto Y.; Nashimoto H.;
 RA Oyama T.; Saito N.; Saito Y.; Sampei G.; Satoh Y.; Sivaasundaram S.;
 RA Tagami H.; Takashashi A.; Takeeda J.; Uehara K.; Wada C.;
 RA Yamagata S.; Horiiuchi T.;
 RT "Construction of a contiguous 874-kb sequence of the *Escherichia coli* K12 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features."ⁿ
 RL DNA Res. 4:91-113 (1997).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=K12; MEDLINE#=9349980; PubMed=9205837;
 RA Yamanoto Y.; Aiba H.; Baba T.; Hayashi K.; Inada T.; Isono K.;
 RA Itoh T.; Kimura S.; Kitagawa M.; Makino K.; Miki T.; Mitsuhashi N.;
 RA Mizobuchi K.; Mori H.; Nakade S.; Nakamoto Y.; Nashimoto H.;
 RA Oyama T.; Saito N.; Saito Y.; Sampei G.; Satoh Y.; Sivaasundaram S.;
 RA Tagami H.; Takashashi A.; Takeeda J.; Uehara K.; Wada C.;
 RA Yamagata S.; Horiiuchi T.;
 RT "Construction of a contiguous 874-kb sequence of the *Escherichia coli* K12 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features."ⁿ
 RL DNA Res. 4:91-113 (1997).
 RN [4]

RP TOPOLOGY.
 RX MEDLINE#=89039254; PubMed=3141744;
 RA Goett P.; Boos W.;
 RT "The transmembrane topology of the sn-glycerol-3-phosphate permease of *Escherichia coli* analysed by phoA and lacZ protein fusions."ⁿ
 RL Mol. Microbiol. 2:555-563 (1988).
 CC -1- FUNCTION: Responsible for glycerol-3-phosphate uptake.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -1- SIMILARITY: Belongs to the major facilitator (MFS) superfamily.
 CC -1- SLC37A family.
 CC

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CC DR Y00536; CAA65598.1; -.
 DR EMBL; AE000314; AACY5300.1; -.
 DR EMBL; D90855; BAA1059.1; -.
 DR PIR; S00888; JNECGT.
 DR Ecogene; EG10401; GIPT.
 DR InterPro; IPR005267; GIPT_transporter.
 DR InterPro; IPR000849; GIPT_transporter.
 DR TIGRFAMS; TIGR00711; MFS.
 DR TIGRFAMS; TIGR000881; 2AG104.1.
 DR TIGRFAMS; TIGR000712; GIPT.1.
 DR PROSITE; PS00442; GIPT.1.
 DR PROSITE; PS50500; MFS; 1.
 KW Glycerol metabolism; Transmembrane; Inner membrane; Transport; Complete proteome.
 KW DOMAIN 1 27
 FT TRANSMEM 28 44
 FT DOMAIN 45 64
 FT TRANSMEM 65 87
 FT DOMAIN 88 95
 FT TRANSMEM 96 113
 FT DOMAIN 114 119
 FT TRANSMEM 120 136
 FT DOMAIN 137 169
 FT TRANSMEM 170 184
 FT DOMAIN 190 190

RT CYTOPLASMIC (PROBABLE).
 RT 6 (PROBABLE).
 RT CYTOPLASMIC (PROBABLE).
 RT 7 (PROBABLE).
 RT PERIPLASMIC (PROBABLE).
 RT 8 (PROBABLE).
 RT CYTOPLASMIC (PROBABLE).
 RT 9 (PROBABLE).
 RT PERIPLASMIC (PROBABLE).
 RT 10 (PROBABLE).
 RT CYTOPLASMIC (PROBABLE).
 RT 11 (PROBABLE).
 RT PERIPLASMIC (PROBABLE).
 RT 12 (PROBABLE).
 RT CYTOPLASMIC (PROBABLE).
 SQ SEQUENCE 452 AA: 50310 MW: QDE70D08D40AD45 CRC64;

SEQUENCE FROM N.A.
 RC STRAIN=K12; MEDLINE#=9278503;
 RA Itoh T.; Kimura S.; Kitagawa M.; Makino K.; Miki T.; Mitsuhashi N.;
 RA Mizobuchi K.; Mori H.; Nakade S.; Nakamoto Y.; Nashimoto H.;
 RA Oyama T.; Saito N.; Saito Y.; Sampei G.; Satoh Y.; Sivaasundaram S.;
 RA Tagami H.; Takashashi A.; Takeeda J.; Uehara K.; Wada C.;
 RA Yamagata S.; Horiiuchi T.;
 RT "Construction of a contiguous 874-kb sequence of the *Escherichia coli* K12 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features."ⁿ
 RL DNA Res. 4:91-113 (1997).
 RN [4]

Query Match 47.6%; Score 39; DB 1; Length 452;
 Best Local Similarity 42.9%; Pred. No. 27;
 Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY	1 CAWYARGIREVGR 14
	: : : :
Db	130 CGWFQGMGWPFCGR 143

RESULT 15
 HMT2_SCHPO STANDARD; PRT; 459 AA.
 ID HMT2_SCHPO STANDARD; PRT; 459 AA.
 AC 094294; O13293 (Rel. 41; Created)
 DT 28-FEB-2003 (Rel. 41; Last sequence update)
 DE Sulfide:quinone oxidoreductase, mitochondrial precursor (EC 1.5.1.1.)
 DB (Heavy metal tolerance protein 2) (Cadmium resistance protein 1).
 GN HMT2 OR CAD1 OR SPBC2G5_06C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Fungi; Ascomycota; Schizosaccharomycetidae;
 OC Schizosaccharomyces; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OC NCBI_TaxID=4896;
 OX

RN [1] -
 RN SEQUENCE FROM N.A., FUNCTION, COFACTOR, SUBCELLULAR LOCATION, AND VARIANT ANALYSIS.
 RP RP VARIANT ANALYSIS.
 RX MEDLINE#=99240711; PubMed=10224084;
 RA Vande Wege J.G.; Ow D.W.; RT "A fission yeast gene for mitochondrial sulfide oxidation.";
 RL J. Biol. Chem. 274:13250-13257 (1999).
 RN [2] -
 RN SEQUENCE FROM N.A.
 RA Mutch N.; Kawabata M.; Nakagawa C.; Yamada K.; RT "Molecular cloning of the gene involved in cadmium sensitivity of fission yeast Schizosaccharomyces pombe.";
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [3] -
 RN SEQUENCE FROM N.A.
 RP RP STRAIN=972; MEDLINE#=2-84841; PubMed=11859360;
 RX RA Wood V.; Gwilliam R.; Hayles J.; Baker S.; Bowman S.; SGouras J.; Peat N.; Jones L.; Leathier S.; McLean J.; RA Brooks K.; Brown D.; Brown S.; Chillingworth T.; Churcher C.M.; RA Collins M.; Connor R.; Cronin A.; Davis P.; Feilwell T.; Hodgetts B.; RA Gertes S.; Goble A.; Hamlin N.; Harris D.; Hidalgo J.; Hodgson G.; RA Holroyd S.; Hornsby T.; Howarth S.; Huckle E.J.; Hunt S.; Jigges K.; RA James K.; Jones L.; Jones M.; Leathier S.; McLean J.; RA Mooney P.; Moule S.; Marsall K.; Murphy L.; Niblett D.; Odeil C.; RA Oliver K.; O'Neil S.; Pearson D.; Quail M.A.; Rabinowitz E.; RA Rutherford K.; Rutter S.; Saunders D.; Seeger G.; Sharp S.; RA Skelton J.; Simmonds M.; Squares R.; Squares S.; Stevens K.; RA Taylor K.; Taylor R.G.; Tivey A.; Walsh S.V.; Warren T.; Whitehead S.; RA Woodward J.; Volkert J.; Aert R.; Robb J.; Gromponez B.; RA Weltens I.; Vanstreels E.; Rieger M.; Schaefer M.; Mueller-Auer S.; RA Gabel C.; Fuchs M.; Fritze C.; Holzer E.; Moestl D.; Hilbert H.; RA Borzym K.; Langer I.; Beck A.; Lehrach H.; Reinhardt R.; Pohl T.M.,

Eger P., Zimmermann W., Weddler H., Wambutt R., Purnelle B., Capela D., Barloy-Hubler F., Gouzy J., Borhe G., Ampe F., Barut J., Boitard P., Becker A., Boutay M., Cadieu B., Gloux S., Godrie T., Goffeau A., Kahn D., Dreano S., Lelaiure V., Masly D., Lucas M., Rochet M., Gailardin C., Tallada V.A., Garzon A., Rhode G., Daga R.R., Cruzado L., Jimenez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forshburg S.L., Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shapovalski G.V., Ussery D., Barrell B.G., Nurse P.; RT "The genome sequence of Schizosaccharomyces pombe.", Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001). RT FUNCTION: INVOLVED IN THE PRODUCTION OF BETA-(1,2)-GLUCAN. RT IT IS INVOLVED NOT ONLY IN INVASION BUT ALSO IN BACTERIOPHYTIC DEVELOPMENT.

CC SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.

CC SIMILARITY: TO A TIMEFACTORS CHVB.

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CC COFACTOR: FAD; noncovalently bound.

CC SUBCELLULAR LOCATION: Mitochondrial.

CC -1- CATION: Ref.2 sequence differs from that shown extensively due to frame-shifts and other sequencing errors.

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DR EMBL: AL033385; CA21B882.1; DR EMBL: BAA22793.1; ALT SEQ. DR EMBL: AF042283; Aad41159.1; -. DR PIR: T433558; T433558.

DR GenDB; SPombe; SFB2CGE_06c7; .

KW Oxidoreductase; Flavoprotein; FAD; NADP; Mitochondrion;

KW TRANSIT peptide; Cadmium. FT TRANSIT 1 24 MITOCHONDRION (POTENTIAL). FT CHAIN 25 459 SULFIDE:QUINONE OXIDOREDUCTASE. FT BIND 30 60 FAD (ADP PART) (POTENTIAL).

FT DISULFID 204 383 REDOX-ACTIVE (BY SIMILARITY).

FT VARIANT 396 396 E -> K (IN CADMIUM SENSITIVE STRAIN).

SEQUENCE 459 AA; 51575 MW; 121F06DCC9579C04 CRC64;

Query Match Score 47.6%; Best Local Similarity 66.7%; Matches 6;保守性 3; 残基 11; 3 WIASRGIRPV 12

Db 445 WTGSRGLIP 453

RESULT 16

RN T7S3_HUMAN STANDARD; PRT; 570 AA.

RN Q9N53; Q9NU44; AC 41; Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Transmembrane 7 superfamily protein member 3 precursor (Seven span TM7SF3.

OS Homo sapiens (Human).

OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606; [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=20291015; PubMed=10828615;

RA Akashi H., Han H.-J., Tizuka M., Nakajima Y., Furukawa Y., Sugano S., Imai K., Nakamura Y.; RT "Isolation and characterization of a novel gene encoding a putative seven-span transmembrane protein, TM7SF3.", RT Cytogenet. Cell Genet. 8:305-309 (2000). [2]

RN SEQUENCE FROM N.A.

RC TISSUE=Placenta; RA Isozai T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki A., Shiratori A., Sudo H., Nishikawa T., Nagai K., Sugano S., [12]

RN SEQUENCE FROM N.A.

RC STRAIN=1021; RA MEDLINE=21336507; PubMed=11481430; RX

RA Waga-tsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watatabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Matsuo Y.,
 RA Niromiya K., Iwayanagi T.;
 RA "NEDO human cDNA sequencing project.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

[3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Straubberg R.L., Feingold E.A., Buetow K.H., Shemmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Jordan H., Marszina K., Farmer A.A., Rubin G.M., Hong L., Diachenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J., Bosak S.A., McLean P.J., McKernan K.J.A., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman J., Madan A., Rodiguez S., Sanchez A., Whiting M., Madan A., Young A.C., Tsoi Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Greenwood J., Schmutz J., Meyers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnierch A., Schein J.E., Jones S.J.M., Matra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -|- SUBCELLULAR LOCATION: Integral membrane protein; Plasma membrane.

CC -|- TISSUE SPECIFICITY: Ubiquitous. The highest expression is in kidney.

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 CC EMBL: AB02470; BA92856.1;
 DR EMBL; AK02031; BA92046.1;
 DR EMBL; BC005176; AAH05176.1;
 DR Genew; HGNC:23049; TM7SP3.
 DR MIM: 605181;
 KW SIGNAL; Transmembrane.
 FT SIGNAL 1 21
 FT CHAIN 22 570 TRANSMEMBRANE 7 SUPERFAMILY PROTEIN MEMBER 3.
 FT TRANSMEM 296 313 POTENTIAL.
 FT TRANSMEM 320 342 POTENTIAL.
 FT TRANSMEM 347 369 POTENTIAL.
 FT TRANSMEM 371 393 POTENTIAL.
 FT TRANSMEM 408 430 POTENTIAL.
 FT TRANSMEM 437 459 POTENTIAL.
 FT TRANSMEM 479 501 POTENTIAL.
 FT DOMAIN 297 327 PHE-RICH.
 FT CARBOHYD 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 264 264 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 564 570 AA; 64166 MW; CC296D7C22AD894C CRC64;

RESULT 18	TIM2-CHICK	STANDARD	PRT	220 AA.
AC 042146;	AC	042146;	AC	042146;
DT 15-JUL-1998 (Rel. 36, Created)	DT	15-JUL-1998 (Rel. 36, Last sequence update)	DT	15-JUL-1998 (Rel. 43, Last annotation update)
DT 15-Mar-2004 (Rel. 43, Last annotation update)	DT	DE Metalloproteinase inhibitor 2 precursor (TIMP-2)	DE metalloproteinases-2).	DE metalloproteinases-2).
GN Gallus Gallus (Chicken).	GN	OS Gallus Gallus (Chicken).	OS	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RA Ames R.T.; Li L.H.; Weaver B.; Hawkes S.; Hahn-Danton E.A., Quigley J.P.; Ra RT inhibitor of metalloproteinase-2 (TIMP-2) in normal and transformed chicken embryo fibroblasts.";	RA	RA Ames R.T.; Li L.H.; Weaver B.; Hawkes S.; Hahn-Danton E.A., Quigley J.P.; Ra RT inhibitor of metalloproteinase-2 (TIMP-2) in normal and transformed chicken embryo fibroblasts.";	RA	CC FUNCTION: Complexes with metalloproteinases (such as collagenases) and irreversibly inactivates them (By similarity).
RL J. Cell. Physiol. 174:342-352 (1998).	RL	CC SUBCELLULAR LOCATION: TIM2 is dependent on the presence of disulfide bonds.	CC	CC - - SUBCELLULAR LOCATION: Belongs to the TIMP family.
CC - - SIMILARITY: Contains 1 NTR domain.	CC	CC - - SIMILARITY: Contains 1 NTR domain.	CC	CC - - SIMILARITY: Belongs to the TIMP family.
CC	CC	CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC DR EMBL; AF004664; AAB69168.1; -.	CC DR EMBL; AF004664; AAB69168.1; -.	CC DR HSSP; P16035; 2TM1.	CC DR InterPro; IPR01820; TIMP.	CC DR InterPro; IPR08993; TIMP_like.
CC DR Pfam; PF00965; TIMP_1.	CC DR SMART; SM00206; NTR_1.	CC DR PROSITE; PS00288; TIMP_1.	CC DR PROSITE; PS00288; TIMP_1.	CC DR PROSITE; PS00288; TIMP_1.
CC FT SIGNAL 1 26 METALLOPROTEINASE INHIBITOR_2.	CC FT SIGNAL 1 26 METALLOPROTEINASE INHIBITOR_2.	CC FT SIGNAL 1 26 METALLOPROTEINASE INHIBITOR_2.	CC FT SIGNAL 1 26 METALLOPROTEINASE INHIBITOR_2.	CC FT SIGNAL 1 26 METALLOPROTEINASE INHIBITOR_2.
CC FT DOMAIN 27 220 NTR.	CC FT DOMAIN 27 220 NTR.	CC FT DOMAIN 27 220 NTR.	CC FT DOMAIN 27 220 NTR.	CC FT DOMAIN 27 220 NTR.
CC FT DISULFID 27 98 BY SIMILARITY.	CC FT DISULFID 27 98 BY SIMILARITY.	CC FT DISULFID 27 98 BY SIMILARITY.	CC FT DISULFID 27 98 BY SIMILARITY.	CC FT DISULFID 27 98 BY SIMILARITY.
CC FT PHE-RICH 39 152 BY SIMILARITY.	CC FT PHE-RICH 39 152 BY SIMILARITY.	CC FT PHE-RICH 39 152 BY SIMILARITY.	CC FT PHE-RICH 39 152 BY SIMILARITY.	CC FT PHE-RICH 39 152 BY SIMILARITY.
CC FT DISULFID 154 201 BY SIMILARITY.	CC FT DISULFID 154 201 BY SIMILARITY.	CC FT DISULFID 154 201 BY SIMILARITY.	CC FT DISULFID 154 201 BY SIMILARITY.	CC FT DISULFID 154 201 BY SIMILARITY.
CC FT DISULFID 159 164 BY SIMILARITY.	CC FT DISULFID 159 164 BY SIMILARITY.	CC FT DISULFID 159 164 BY SIMILARITY.	CC FT DISULFID 159 164 BY SIMILARITY.	CC FT DISULFID 159 164 BY SIMILARITY.
CC SQ SEQUENCE 220 AA; 64166 MW; CC296D7C22AD894C CRC64;	CC SQ SEQUENCE 220 AA; 64166 MW; CC296D7C22AD894C CRC64;	CC SQ SEQUENCE 220 AA; 64166 MW; CC296D7C22AD894C CRC64;	CC SQ SEQUENCE 220 AA; 64166 MW; CC296D7C22AD894C CRC64;	CC SQ SEQUENCE 220 AA; 64166 MW; CC296D7C22AD894C CRC64;
Query Match 47.0%; Score 38.5%; DB 1; Length 570;	Query Match 46.3%; Score 38; DB 1; Length 220;	Query Match 46.3%; Score 38; DB 1; Length 220;	Query Match 46.3%; Score 38; DB 1; Length 220;	Query Match 46.3%; Score 38; DB 1; Length 220;
Best Local Similarity 53.8%; Pred. No. 41; Indels 1; Gaps 1;	Best Local Similarity 63.6%; Pred. No. 20; Mismatches 1; Gaps 1;	Best Local Similarity 63.6%; Pred. No. 20; Mismatches 1; Gaps 1;	Best Local Similarity 63.6%; Pred. No. 20; Mismatches 1; Gaps 1;	Best Local Similarity 63.6%; Pred. No. 20; Mismatches 1; Gaps 1;
Matches 7; Conservative 7; Mismatches 2; Gaps 1;	Matches 7; Conservative 7; Mismatches 2; Gaps 1;	Matches 7; Conservative 7; Mismatches 2; Gaps 1;	Matches 7; Conservative 7; Mismatches 2; Gaps 1;	Matches 7; Conservative 7; Mismatches 2; Gaps 1;
Qy 1 CAWYASRGIRPV 11	Qy 1 CAWYASRGIRPV 11	Qy 1 CAWYASRGIRPV 11	Qy 1 CAWYASRGIRPV 11	Qy 1 CAWYASRGIRPV 11
Db 201 CAWY-RGMNP 209	Db 201 CAWY-RGMNP 209	Db 201 CAWY-RGMNP 209	Db 201 CAWY-RGMNP 209	Db 201 CAWY-RGMNP 209

RESULT 19		CBPB_BOVIN	STANDARD	PRT;	306 AA.
CAL2_PARTE	STANDARD;				
ID : CAL2_PARTE					
AC : Q34715;					
DT : 28-FEB-2003 (Rel. 41; Created)					
DT : 28-FEB-2003 (Rel. 41; Last sequence update)					
DT : 28-FEB-2003 (Rel. 41; Last annotation update)					
DE : Putative cathepsin L2 (EC 3.4.22.15) (Fragment).					
OS : Paramecium tetraurelia.					
OC : Alveolata; Ciliophora; Oligohymenophorea; Peniculida;					
NCBI_TaxID:5888;					
RN : [1]					
RP : SEQUENCE FROM N.A.					
RC : STRAIN=Stock 51;					
RX : MEDLINE=1624439; PubMed=865938;					
RA : Voeikov H., Kurz U., Linder J., Klunpp S., Gnau V., Jung G.,					
RA : Schultz J.E.,					
RT : "Cathepsin L is an intracellular and extracellular protease in					
RT : Paramecium tetraurelia: Purification, cloning, sequencing and specific					
RR : inhibition by its expressed propeptide.";					
RL : Bur. J. Biochem. 238:198-206(1996).					
-!- FUNCTION: May be involved in extracellular digestion.					
-!- CATALYTIC ACTIVITY: Specificity close to that of papain. As					
CC : compared to cathepsin B, cathepsin L exhibits higher activity					
CC : towards protein substrates, but has little activity on Z-Arg-Arg-					
CC : NH ₂ , and no peptidyl-dipeptidase activity.					
CC : SUBCELLULAR LOCATION: Secreted.					
CC : -!- SIMILARITY: Belongs to peptidase family Cl.					
CC : -!- CATION: This protein may be non-functional as it lacks the					
CC : cysteine active site residue which is replaced by Gly-118.					
CC : -----					
CC : This SWISS-PROT entry is copyright. It is produced through a collaboration					
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CC : entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
CC : -----					
DR : EMBL; X91756; CAK62871.1; -.					
DR : PIR; S68784; S68784.					
DR : HSSP; O0911; 1FHO.					
DR : InterPro; IPR000668; Peptidase_C1.					
DR : InterPro; IPR000169; SProte_acsite.					
DR : Pfam; PF001112; Peptidase_C1; 1.					
DR : ProDom; PD000158; Peptidase_C1; 1.					
DR : SMART; SM00645; Pept_C1; 1.					
DR : PROSITE; PS00640; THIOL PROTEASE ASN; FALSE NEG.					
DR : PROSITE; PS00139; THIOL PROTEASE CYS; FALSE NEG.					
DR : PROSITE; PS00639; THIOL PROTEASE HIS; FALSE NEG.					
KW : Hydrolase; thiol protease.					
FT : NON_TER; 1	1				
FT : PROTEP; <1	?				
FT : CHAIN; ?	294				
FT : SITE; 118	118				
FT : ACT_SITE; 247	247				
FT : ACT_SITE; 264	264				
FT : DISULFID; 240	284				
SQ : SEQUENCE; 294 AA;	33627 MW;	6FD688A0176BEC51 CRC64;			
Query Match	46.3%	Score 38; DB 1; Length 294;			
Best Local Similarity	54.5%	Pred. No. 27;			
Matches	6;	Conservative			
2 AWYASRGIRPV 12	2;	Mismatches	3;	Indels	0;
: :					
Db	129 ANTAIRGQRKI 139				
RESULT 20					
CBPB_BOVIN					

QY	1 CAYWASRGURPVGR 14	FT	METAL	236	236	IRON (HEM 3 AXIAL LIGAND)
Db	76 CQWFVREAVRTYGR 89	FT	BINDING	247	247	HEM 3 (COVALENT) (BY SIMILARITY).
		FT	BINDING	250	250	HEM 3 (COVALENT) (BY SIMILARITY).
		FT	METAL	251	251	IRON (HEM 3 AXIAL LIGAND) (BY SIMILARITY).
		FT	BINDING	307	307	HEM 4 (COVALENT) (BY SIMILARITY).
		FT	BINDING	310	310	HEM 4 (COVALENT) (BY SIMILARITY).
		FT	METAL	311	311	IRON (HEM 4 AXIAL LIGAND) (BY SIMILARITY).
RESULT 21		SQ	SEQUENCE	383 AA;	Score 38;	DB 1; Length 383;
CYCR CHRVI STANDARD;	PRT;	383 AA;	Query Match 46.3%; Best Local Similari	35;	Score 38;	DB 1; Length 383;
AC ID: CYCR CHRVI	AC	30-MAY-2000 (Rel. 39, Created)	ID: CBPB_HUMAN	3; Mismatches	Pred. No. 35;	PRT; 417 AA.
DT 30-MAY-2000 (Rel. 39, Last sequence update)	RA	Qin H., Allen R., Knaff D.B.;	ID: P15086; Q96SQ8;	4; Indels	0;	
DT 10-OCT-2003 (Rel. 42, Last annotation update)	RA	"Primary structure of genes encoding light-harvesting and reaction center proteins from Chromatium vinosum;"	DT: 01-APR-1990 (Rel. 14, Created)	Gaps	0;	
DE Photosynthetic reaction center cytochrome C subunit precursor.	RA	Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.	DT: 28-FEB-2003 (Rel. 41, Last sequence update)			
GN PUFc.	RA	-!- FUNCTION: THE REACTION CENTER OF PURPLE BACTERIA CONTAIN A TIGHTLY BOUND CYTOCHROME MOLECULE WHICH RE-DUCES THE PHOTO OXIDIZED PRIMARY ELECTRON DONOR.	DT: 10-OCT-2003 (Rel. 42, Last annotation update)			
OS Chromatiaceae; Prokaryotae; Gammaproteobacteria; Chromatiales; Bacteria; Protobacteria; Gammaproteobacteria; Chromatiales; Chromataceae; Allochromatium.	RA	-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (By similarity)	DE: Carboxypeptidase B precursor (EC 3.4.17.2) (Pancreas-specific protein)			
OC NCBI_TaxID:1049;	RA	CC 4- Binds 4 heme groups per molecule.	DE: Carboxypeptidase B precursor (EC 3.4.17.2) (Pancreas-specific protein)			
OX RN	RA	-!- SIMILARITY: HIGH, WITH OTHER PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNITS.	DE: Carboxypeptidase B precursor (EC 3.4.17.2) (Pancreas-specific protein)			
CC	RA	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).	DE: Carboxypeptidase B precursor (EC 3.4.17.2) (Pancreas-specific protein)			
CC	RA	EMBL: AB011811; BAA32742; 1; HSSP; P07173; GPRC.	DR: IPR000345; Cytc_heme_BS.	RN	SEQUENCE FROM N.A.	
CC	RA	InterPro: IPR003158; Cytc_RC.	DR: InterPro; IPR003158; Cytc_RC.	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
CC	RA	PFam: PF02276; Cytc_RC.	DR: PF02276; Cytc_RC.	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
CC	RA	ProDom: P001001; Cytc_RC.	DR: ProDom; P001001; Cytc_RC.	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
CC	RA	PROSITE: PS00190; CYTOCHROME_C_4.	DR: PROSITE; PS00190; CYTOCHROME_C_4.	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
CC	RA	Electron Transport; Photosynthesis; Reaction center; Heme Membrane; Lipoprotein; Repeat; Signal; Palmitate.	DR: Electron Transport; Photosynthesis; Reaction center; Heme Membrane; Lipoprotein; Repeat; Signal; Palmitate.	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
CC	RA	SIGNAL 1 22 BY SIMILARITY.	FT: SIGNAL 1 22 BY SIMILARITY.	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
CC	RA	CHAIN 23 383 PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT.	FT: CHAIN 23 383 PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT.	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
FT	PT	LIPID 23 23 S-diacylglycerol cysteine (By similarity).	FT: LIPID 23 23 N-palmitoyl cysteine (By similarity).	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
FT	PT	METAL 94 94 IRON (HEM 1 AXIAL LIGAND) (BY SIMILARITY).	FT: METAL 94 94 IRON (HEM 1 AXIAL LIGAND) (BY SIMILARITY).	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
FT	PT	BINDING 107 107 HEME 1 (COVALENT) (BY SIMILARITY).	FT: BINDING 107 107 HEME 1 (COVALENT) (BY SIMILARITY).	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
FT	PT	BINDING 110 110 IRON (HEM 1 AXIAL LIGAND) (BY SIMILARITY).	FT: BINDING 110 110 IRON (HEM 1 AXIAL LIGAND) (BY SIMILARITY).	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
FT	PT	METAL 111 111 IRON (HEM 2 AXIAL LIGAND) (BY SIMILARITY).	FT: METAL 111 111 IRON (HEM 2 AXIAL LIGAND) (BY SIMILARITY).	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
FT	PT	METAL 130 130 IRON (HEM 4 AXIAL LIGAND) (BY SIMILARITY).	FT: METAL 130 130 IRON (HEM 4 AXIAL LIGAND) (BY SIMILARITY).	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
FT	PT	METAL 144 144 IRON (HEM 4 AXIAL LIGAND) (BY SIMILARITY).	FT: METAL 144 144 IRON (HEM 4 AXIAL LIGAND) (BY SIMILARITY).	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
FT	PT	BINDING 152 152 HEME 2 (COVALENT) (BY SIMILARITY).	FT: BINDING 152 152 HEME 2 (COVALENT) (BY SIMILARITY).	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
FT	PT	BINDING 155 155 HEME 2 (COVALENT) (BY SIMILARITY).	FT: BINDING 155 155 HEME 2 (COVALENT) (BY SIMILARITY).	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	
FT	PT	METAL 156 156 IRON (HEM 2 AXIAL LIGAND) (BY SIMILARITY).	FT: METAL 156 156 IRON (HEM 2 AXIAL LIGAND) (BY SIMILARITY).	RC	SEQUENCE FROM N.A., AND SEQUENCE OF 16-40.	

Wednesday, February 25, 2004 08:04:57 2004

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002). [4]

RN SEQUENCE OF 16-43.

RC TISSUE-Pancreas;

RX MEDLINE=89153096; PubMed=2920728;

RA Pascual R., Burgos F.J., Scriani F., Mendez E., Aviles F.X.; "Purification and properties of five different forms of human procarboxypeptidases"; Eur. J. Biochem. 179:609-616 (1989).

CC -I- CATALYTIC ACTIVITY: Peptidyl-L-lysine(or L-arginine) + H(2)O = peptide + L-lysine(or L-arginine).

CC -I- ISSUE SPECIFICITY: Pancress.

CC -I- SIMILARITY: Belongs to Peptidase family M14.

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CC EMBL; M81057; AA66973.1; -.

DR EMBL; AJ224866; CAA12163.1; -.

DR DR; BC015338; AAH15338.1; -.

DR PDB; 1KWM; 28-AUG-02.

DR MEROPS; M14_003; -.

DR Genew; HGNC-2299; CPB1.

DR MIM; 114852; -.

DR GO; GO0004180; F:carboxypeptidase activity; TAS.

DR InterPro; IPR0003146; Pept_M14A_dropep.

DR InterPro; IPR000834; Peptidase_M14.

DR InterPro; IPR003200; Protease_inhib.

DR Pfam; PF02244; Protop_M14; 1.

DR Pfam; PF00246; ZincCarbOpept; 1.

DR SMART; SM00631; Zinc_Pept_1.

DR PROSITE; PS00132; CARBOXYPT_ZN_1; 1.

DR PROSITE; PS00133; CARBOXYPT_ZN_2; 1.

KW Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Zymogen; Signal; 3D-structure.

KW SIGNAL 1 15 ACTIVATION PEPTIDE.

FT PROPEP 16 110 CARBOXYPEPTIDASE B.

FT CHAIN 111 417 BY SIMILARITY.

FT METAL 176 176 ZINC (BY SIMILARITY).

FT METAL 179 179 ZINC (BY SIMILARITY).

FT METAL 304 304 ZINC (BY SIMILARITY).

FT ACT SITE 378 378 NUCLEOPHILE (BY SIMILARITY).

FT DISULFID 173 186 BY SIMILARITY.

FT DISULFID 245 268 BY SIMILARITY.

FT DISULFID 259 273 BY SIMILARITY.

FT CONFLICT 16 16 H > A (IN REF. 1; AA SEQUENCE) .

FT CONFLICT 17 17 H > Q (IN REF. 1; AA SEQUENCE) .

FT CONFLICT 37 37 H > Q (IN REF. 4) .

FT CONFLICT 208 208 D > N (IN REF. 2) .

FT CONFLICT 245 245 MISSING (IN REF. 1).

SQ SEQUENCE 417 AA; 47367 MW; EBBBB98B27F5DSAF9 CRC64;

Query Match Best Local Similarity 35.7%; Pred. No. 37; Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0; RESULT 24

Qy 1 CAYASRGIRPVGR 14

Db 186 CWFVREAVRVTYGR 199

RESULT 23

ENO_MYCPU

DR TIGERAMS; TIGR01123; ilvE_III; 1.
 DR PROSITE; PS00770_AA_TRANSFER; CLASS_4; 1.
 KW Pyridoxal Aminotransferase; Branched-chain amino acid biosynthesis;
 KW Pyridoxal Phosphate (BY SIMILARITY).
 PT BINDING 244 244 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 PT CONFLICT 86 86 D -> I (IN REF. 2).
 PT CONFLICT 118 118 F -> FS (IN REF. 2).
 PT CONFLICT 154 170 DEDSEEMINVTELLRL -> VFLRGDDQCTYRLS
 PT CONFLICT 391 397 MKFVNT -> RKLQHN (IN REF. 2).
 SQ SEQUENCE 415 AA; 47341 MW; AE215FC9623FB390 CRC64;
 Query Match 45.7%; Score 37.5; DB 1; Length 415;
 Best Local Similarity 44.4%; Pred. No. 46;
 Matches 8; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

Qy 1 CAWYASR-----IRPYG 13
 Db 83 CDWDAERGWHHPXLEPIG 100

RESULT 26
 ID R157_BOVIN STANDARD; PRT; 147 AA.
 AC Q28183_1
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Retina specific 15.7 kDa protein.
 OS Bos taurus (Bovine).
 EC Eukaryote; Mucozyme; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Bovidae; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N_A.
 RC TISSUE-Retina;
 RX MEDLINE=862581668; PubMed=2425311;
 RA Nakagawa Y., Kuo C.H., Ishii K., Shiosaka S., Tohyama M., Miki N.;
 RT "Cloning and characterization of a cDNA specific for bovine retina.";
 RL Neurosci. Res. 3:309-310(1986).
 CC - - TISSUE SPECIFICITY: Retina.
 CC - -

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 DR PIR: I45978; I45978.
 SQ SEQUENCE 147 AA; 15658 MW; 1FED48788B39645 CRC64;

Query Match 45.1%; Score 37; DB 1; Length 147;
 Best Local Similarity 71.4%; Pred. No. 20;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAWYASR 7
 Db 100 CSWFASR 106

RESULT 27
 ID Y064_TREPA STANDARD; PRT; 191 AA.
 AC 083103_1
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein TP0064.

CC - - PATHWAY: Biosynthesis of lysine from aspartate semialdehyde; sixth step.

CC - - SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

Treponema pallidum.
 Bacteria; Spirochaetes; Spirochaetales; Treponematales;
 NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N_A.

RC STRAIN=Nichols;
 RX MEDLINE=9833270; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwynn M., McLeod M.P., Salzberg S., Peterson J.J., Sodergren E., Hardman J.M., Richardson E., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.
 RA "Complete genome sequence of *Treponema pallidum*, the syphilis spirochete." Science 281:375-388 (1998).

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 DR PIR: I45978; H71370; H71370.

DR EMBL; AE001191; AAC65064; 1; -.
 DR PIR: TP0064; -.
 DR PIR: H71370; H71370.

KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 191 AA; 22079 MW; 2837931F910CD831 CRC64;
 DR PIR: H71370; H71370.

Query Match 45.1%; Score 37; DB 1; Length 191;
 Best Local Similarity 57.1%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAWYASR-----IRPYG 14
 Db 16 CAPYGRGEPPVRR 29

RESULT 28

DR PIR: H71370; STANDARD; PRT; 257 AA.
 ID DAPF_CHLTETE STANDARD; PRT; 257 AA.
 AC Q8KX9;
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 DR PIR: H71370; H71370.

DR PIR: TP0064; 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Diaminopimelate epimerase (EC 5.1.1.7) (DAP epimerase).
 GN DAPF OR CT2021;
 OS *Chlorobium tepidum*.
 CC Bacteria; Chlorobi; Chlorobia; Chlorobiaceae;
 CC Chlorobium.
 OX NCBI_TaxID=10977;
 RN [1]
 RP SEQUENCE FROM N_A.
 RC STRAIN=TLS / ATCC 49652 / DSM 12025;
 RX MEDLINE=2103685; PubMed=1203901;
 RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M., Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H., Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F., Holt I., Umayam L.A., Mason T., Brenner M., Shoa T.P., Parksey D., Nieman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D., Vaishnavi J., Khouri H., White O., Gruber T.M., Kerlach K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
 RA "The complete genome sequence of *Chlorobium tepidum* TLS, a photosynthetic, anaerobic, green sulfur bacterium." Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
 CC - ! CATALYTIC ACTIVITY: LL-2,6-diaminoheptanedioate = meso-
 CC - ! diaminohexanedioate
 CC - ! PATHWAY: Biosynthesis of lysine from aspartate semialdehyde; sixth step.
 CC - ! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: Belongs to the diaminodimelate epimerase family.

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CC CC

CC EMBL: U3273; AAC22182.1; .

CC DR PIR: C64074; C64074.

CC DR HSSP: P11604; 1B57.

CC DR TIGR: HIG024.

CC DR InterPro: IPR006411; Fruct_bisP_bact.

CC DR Pfam: PF01116; F bp aldolase.

CC DR ProDom: PD002376; K_bp aldolase; 1.

CC DR TIGR4AMS: TIGR01520; Prubisaldo II A; 1.

CC DR TIGR4AMS: TIGR01520; Prubisaldo II CLASS-II-1; 1.

CC DR PROSITE: PS00622; ALDOLASE-CLASS-II-1; 1.

CC DR PROSITE: PS00866; ALDOLASE-CLASS-III-2; 1.

CC DR TIGR4AMS; TIGR0655; DAP; 1.

CC DR PROSITE; PS01126; DAP EPIMERASE; FALSE NEG.

KW Isomerase; Lysine biosynthesis; Complete proteome.

FT ACT SITE 66 BY SIMILARITY.

FT ACT SITE 66 BY SIMILARITY.

FT ACT SITE 198 198 BY SIMILARITY.

FT ACT SITE 28052 MN; A25BD74CE3AEB9AS CRC64;

SQ SEQUENCE 257 AA; 359 AA; 28052 MN; A25BD74CE3AEB9AS CRC64;

Query Match Score 45.1%; Score 37; DB 1; Length 359;

Best Local Similarity 56.2%; Pred. No. 35; Mismatches 2; Indels 2; Gaps 0;

Matches 9; Conservative 2; Mismatches 3; Indels 2; Gaps 2; Indels 0; Gaps 0;

Qy 1 CA-WYASR-GIRPVYR 14

Db 72 CAVVFAHLIGRPGK 87

RESULT 29

ALR1_RHIL0 STANDARD; PRT; 359 AA.

ID ALR1_RHIL0 STANDARD; PRT; 397 AA.

AC 098A5; .

AC DR 28-FEB-2003 (Rel. 41, Created)

AC DR 28-FEB-2003 (Rel. 41, Last sequence update)

AC DR 28-FEB-2003 (Rel. 41, Last annotation update)

AC DE Alanine racemase, biosynthetic (EC 5.1.1.1).

AC GN ALR OR MU6211.

AC OS Rhizobium loti (Mesorhizobium loti).

AC OC Bacterium; Proteobacteria; Alphaproteobacteria; Rhizobiales;

AC OC Phyllobacteriaceae; Mesorhizobium.

AC OX NCBI_TaxID=381; [1] -

RN RP SEQUENCE FROM N.A.

RN RX MEDLINE=MAFF303199; PubMed=11214968;

RN RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Itoesawa K., Ishikawa A., Kawashima K., Kimura T., Kohara M., Matsunaga A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpou S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., RT Mesorhizobium loti";

RN RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

RN RT Mesorhizobium loti";

RN RT DNA Res. 7:331-338 (2000).

RN CC -!- FUNCTION: Provides the D-alanine required for cell wall biosynthesis (By similarity).

RN CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.

RN CC -!- COFACTOR: Pyridoxal phosphate (By similarity).

RN CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first step.

RN CC -!- SIMILARITY: Belongs to the alanine racemase family.

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RN CC AP003008; BAB52539_1; .

RN DR EMBL; MF_01201; .

RN DR HAMAP; MF_01201; .

RN DR InterPro; IPR000821; Ala_racemase.

RL "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.", Venter J.C.; Fritchman J.L., Fuhrmann J.L., Georghagen N.S.M., Gnehtil C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.C., RT Phosphate + D-glyceraldehyde 3-phosphate.

CC -!- COFACTOR: Zinc (By similarity).

CC -!- PATHWAY: Glycolysis; sixth step.

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SIMILARITY: Belongs to class II fructose-bisphosphate aldolase family.

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DR	InterPro; IPR009006; Racem_decarbox_C.	DR	InterPro; IPR003593; AAA_ATPase.
DR	InterPro; IPR001608; UPF0001.	DR	InterPro; IPR000897; SRP54.
DR	Pfam; PF00042; Ala_racemase_C; 1.	DR	InterPro; IPR004125; SRP54_SPB.
DR	Pfam; PF01168; Ala_racemase_N; 1.	DR	Pfam; PF00444; SRP54; 1.
DR	PRINTS; PRO0992; ALANINE_RACEMASE.	DR	Pfam; PF02881; SRP54_N; 1.
DR	PROSITE; PS00395; ALANINE_RACEMASE.	DR	Pfam; PF02978; SRP_SPB; 1.
KW	Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis; Complete proteome.	DR	PRODOM; PD000819; SRP54; 1.
KW	CATALYTIC BASE SPECIFIC TO D-ALANINE (BY SIMILARITY).	DR	SMART; SM00322; AAA; 1.
FT ACT_SITE	42 42	DR	PROSITE; PS00300; SRP54; FALSE NEG.
FT ACT_SITE	257 257	KW	Signal recognition particle; GTP-binding; RNA-binding; Complete proteome.
FT BINDING	42 42	KW	G-DOMAIN (BY SIMILARITY).
FT BINDING	397 AA; 43462 MW;	FT DOMAIN	M-DOMAIN (BY SIMILARITY).
SQ SEQUENCE	15996F5136A9C307 CRC64;	FT NP_BIND	GTP (BY SIMILARITY).
Query Match	Score 37;	FT NP_BIND	GTP (BY SIMILARITY).
Best Local Similarity 45.1%;	DB 1; Length 397;	FT NP_BIND	GTP (BY SIMILARITY).
Matches 6; Conservative 60.0%;	Pred. No. 54;	FT DOMAIN	POLY-GLY.
Matches 1; Mismatches 3;	Indels 0;	SQ SEQUENCE	460 AA;
Qy 3 WYASRGRPV 12	Score 37;	Query Match	Length 460;
Db 98 WTRSHGLIPV 107	DB 1;	Best Local Similarity 44.4%;	Prod. No. 62;
		Matches 4;	Mismatches 1;
		Conservative	Indels 0;
		Gaps 0;	Gaps 0;
RESULT 31			
ID SRP54_HALN1	STANDARD;		
AC Q9HMNF;	PRT;	460 AA.	
AC			
DT 16-OCT-2001 (Rel. 40, Created)			
DT 16-OCT-2001 (Rel. 40, Last sequence update)			
DT 10-OCT-2003 (Rel. 42, Last annotation update)			
DE Signal recognition 54 kDa protein (SRP54).			
GN SRP54 OR VNG2459c.			
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).			
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;			
OC Halobacteriaceae; Halobacterium.			
OX NCBI_TaxID=6409;-;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=20514483; PubMed=11016550;			
RX Ng W.V., Kennedy S.P., Maitraias G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Sbrrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauer K., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenberger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Fritas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebbhardt H., Low T.M., Liang P., Riley M., Hood L., Dassarma S., RT "Genome sequence of Halobacterium species NRC-1"; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).			
CC -!- FUNCTION: Binds to the signal sequence of pressecretory protein when they emerge from the ribosomes (By similarity).			
CC -!- SUBUNIT: Archaeal signal recognition particle consists of a 7S RNA molecule of 300 nucleotides and two protein subunits: SRP54 and SRP19 (By similarity).			
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC -!- DOMAIN: Has a two domain structure: the G-domain binds GTP; the M-domain binds the 7S RNA in presence of SRP19 and also binds the signal sequence (By similarity).			
CC -!- SIMILARITY: Belongs to the GTP-binding SRP family.			
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CC EMBL; AF95887; AF95893; AF95893_1; -.			
CC HAMAP; MF_00306; -1.			
CC InterPro; IPR003593; AAA_ATPase.			
CC InterPro; IPR000897; SRP54.			
CC InterPro; IPR004125; SRP54_SPB.			
CC Pfam; PF00448; SRP54; 1.			
CC Pfam; PF02881; SRP54_N; 1.			
CC ProDom; PF02978; SRP_SPB; 1.			
CC DR HAMAP; MF_00306; -1.			
CC DR HSSP; Q07347; 2FPH.			
CC DR HAMAP; MF_00306; -1.			

DR	SMART; SM00382; AAA; 1.	GN	BOP1 OR KIAAC0124.
DR	PROSITE; PS00100; SRP54; FALSE NEG.	OS	Homo sapiens (Human).
KW	Signal recognition particle; GTP-binding; RNA-binding.	OC	Eukaryota; Merazoza; Chordata; Craniata; Vertebrata; Euteleostomi;
FT	DOMAIN 1 289 G-DOMAIN (BY SIMILARITY).	OC	Mammalia; Eutherria; Primates; Catarrhini; Hominidae; Homo.
DOMAIN	290 465 M-DOMAIN (BY SIMILARITY).	NCBI_TAXID	9601;
FT	NP_BIND 104 111 GTP (BY SIMILARITY).	RN	[1]
FT	NP_BIND 184 188 GTP (BY SIMILARITY).	RP	SEQUENCE FROM N.A.
FT	NP_BIND 242 245 GTP (BY SIMILARITY).	RC	TISSUE Brain, Eye, Lymph, Muscle, and Pancreas;
SQ	SEQUENCE 465 AA; 90918 MN; 9F5705838DFF8370 CRC64;	RX	Medline=12477932; PubMed=12477932;
Query Match	Score 37; DB 1; Length 465;	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Best Local Similarity	45.1%; Pred. No. 62;	RA	Klaussner R.D., Collins F.S., Wagner J., Shemesh C.M., Schuler G.D.,
Matches	4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;	RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Qy	3 WYASRGIRP 11	RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Db	120 WFSKKGLRP 128	RA	Diatrichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RESULT 33		RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
NCAP_CCHFV	STANDARD; PRT; 482 AA.	RA	Blacksley R.W., Usain T.B., Carninci P., Prange C.,
ID	AC P27317; DT 01-AUG-1992 (Rel. 23, Created)	RA	Raha S.S., Logueblanc N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
NCAP_CCHFV	DT 01-JUL-1992 (Rel. 23, Last sequence update)	RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunnarson P.H.,
NCAP_CCHFV	DT 01-JUL-1993 (Rel. 26, Last annotation update)	RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
NCAP_CCHFV	DE Nucleocapsid protein (Nucleoprotein).	RA	Villalain D.K., Muzdy D.M., Soderren E.J., Lu X., Gibbs R.A.,
NCAP_CCHFV	DE Crimean-Congo hemorrhagic fever virus (isolate C68031) (CCHFV).	RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
NCAP_CCHFV	OS Viruses; ssRNA negative-strand viruses; Bunyaviridae; Nairovirus.	RA	Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
NCAP_CCHFV	OC NCBI-TaxID=11594;	RA	Blacksley R.W., Touchman J.W., Green E.D., Dickenson M.C.,
NCAP_CCHFV	RN SEQUENCE FROM N.A.	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
NCAP_CCHFV	RX MEDLINE=92315384; PubMed=1641991;	RA	Butterfield Y.S.N., Krzywinski M.I., Skalska R., Smailus D.E.,
NCAP_CCHFV	RA Marriott A.C., Nuttall P.A.;	RA	Schnarch A., Schein J.E., Jones S.J.M., Matra M.A./
NCAP_CCHFV	RT "Comparison of the S RNA segments and nucleoprotein sequences of	RA	RT "Generation and initial analysis of more than 15,000 full-length
NCAP_CCHFV	RT Crimean-Congo hemorrhagic fever, Hazara, and Dugbe viruses."	RA	RT human and mouse cDNA sequences.";
NCAP_CCHFV	RL Virology 189:795-799(1992).	RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
NCAP_CCHFV	CC -1 SUBCELLULAR LOCATION: Internal protein of virus particle.	RN	RN [2]
NCAP_CCHFV	RN SEQUENCE OF 65-746 FROM N.A.	RX	RX
NCAP_CCHFV	RX MEDLINE=96127510; PubMed=8590280;	RA	RA Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N./
NCAP_CCHFV	RA "Prediction of the coding sequences of unidentified human genes. IV.	RA	RA "Prediction of the coding sequences of unidentified human genes. IV.
NCAP_CCHFV	RA "Comparison of the S RNA segments and nucleoprotein sequences of	RA	RA The coding sequences of 40 new genes (KIAA021-KIAA0160) deduced by
NCAP_CCHFV	RA DE Nucleocapsid protein (Nucleoprotein).	RA	RA analysis of cDNA clones from human cell line KG-1.";
NCAP_CCHFV	RA RL Res. 2:167-174(1995).	RL	RA DNA Res. 2:167-174(1995).
NCAP_CCHFV	RN SUBCELLULAR LOCATION.	RN	RN [3]
NCAP_CCHFV	RX MEDLINE=22317277; PubMed=12429849;	RX	RX
NCAP_CCHFV	RA Scherl A., Couet Y., Deon C., Calle A., Kindbeiter K., Sanchez J.-C.,	RA	RA Scherl A., Couet Y., Deon C., Calle A., Kindbeiter K., Sanchez J.-C.,
NCAP_CCHFV	RA Greco A., Hochstrasser D., Diaz J.J./	RA	RA Greco A., Hochstrasser D., Diaz J.J./
NCAP_CCHFV	RA "Functional proteomic analysis of human nucleus.";	RA	RA "Functional proteomic analysis of human nucleus.";
NCAP_CCHFV	RA RL Mol. Biol. Cell 13:4100-4109(2002).	RL	RA Mol. Biol. Cell 13:4100-4109(2002).
NCAP_CCHFV	CC -1 SUBCELLULAR LOCATION: Nuclear, nucleolar.	CC	CC -1 SUBCELLULAR LOCATION: Nuclear, nucleolar.
NCAP_CCHFV	CC -1 SIMILARITY: Contains 7 WD repeats.	CC	CC -1 SIMILARITY: Contains 7 WD repeats.
NCAP_CCHFV	CC -1 SIMILARITY: STRONG, TO YEAST YMR019C.	CC	CC -1 SIMILARITY: STRONG, TO YEAST YMR019C.
NCAP_CCHFV	CC This SWISS-PROT entry is copyright. It is produced through a collaboration	CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
NCAP_CCHFV	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	CC	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
NCAP_CCHFV	CC the European Bioinformatics Institute. There are no restrictions on its	CC	CC the European Bioinformatics Institute. There are no restrictions on its
NCAP_CCHFV	CC use by non-profit institutions as long as its content is in no way	CC	CC use by non-profit institutions as long as its content is in no way
NCAP_CCHFV	CC modified and this statement is not removed. Usage by and for commercial	CC	CC modified and this statement is not removed. Usage by and for commercial
NCAP_CCHFV	CC entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	CC entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
NCAP_CCHFV	CC DR EMBL; B0442888; 1; -	CC	CC DR EMBL; BC001086; AAH01086; 1; ALT_INIT.
NCAP_CCHFV	CC DR PIR; B42990; VHUCH.	CC	CC DR EMBL; BC005160; AAH015160; 1; ALT_INIT.
NCAP_CCHFV	CC DR Int-Prot; IPR003486; Nairo_nucleocap.	CC	CC DR EMBL; BC007274; AAH07274; 1; -.
NCAP_CCHFV	CC DR Pfam; PF02477; Nairo_nucleocap; 1.	CC	CC DR EMBL; BC013787; AAH13787; 1; -.
NCAP_CCHFV	CC DR ProDom; PD006549; Nairo_nucleocap; 1.	CC	CC DR EMBL; BC013980; AAH13980; 1; -.
NCAP_CCHFV	CC KW Nucleocapsid; RNA-binding.	CC	CC DR EMBL; BC017674; AAH17674; 1; -.
NCAP_CCHFV	CC SQ SEQUENCE 482 AA; 53965 MN; 171F8D9438F00FA2 CRC64;	CC	CC DR EMBL; D50914; BAA09473; 1; -.
NCAP_CCHFV	CC DR SWISS-2DPAGE; Q14137; HUMAN.	CC	CC DR Genew; HGNC:15519; BOP1.
NCAP_CCHFV	CC DR InterPro; IPR01680; WD40.	CC	CC DR Pfam; PF00400; WD40; 5.
NCAP_CCHFV	CC DR SMART; SM00320; WD40; 7.	CC	CC DR PROSITE; PS00678; WD_REPEATS_1; 1.
NCAP_CCHFV	CC DR PROSITE; PS50092; WD_REPEATS_2; 2.	CC	CC DR PROSITE; PS50244; WD_REPEATS_REGION; 2.
NCAP_CCHFV	CC DR PROSITE; PS50244; WD_REPEATS_REGION; 2.	CC	CC DR KW Nuclear protein; Repeat; WD repeat.
NCAP_CCHFV	CC DE Block of proliferation 1.	CC	CC DE

Query Match Score 37; DB 1; Length 768;
 Best Local Similarity 75.0%; Prod. No. 1e+02;
 Matches 6;保守性 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YASRGIRP 11
 Db 521 YGSRGVRP 528

RESULT 35
 METE_LACPL STANDARD; PRT; 768 AA.
 AC Q8BX63; CC 1 CAYASRGIRPVG 13
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase
 DE (EC 2.1.14) (Methionine synthase, vitamin-B12 independent isozyme)
 DE (Cobalamin-independent methionine synthase).
 GN METE OR LP_1375.
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIB 8826 / WCP51;
 RX MEDLINE=224B0296; PubMed=12566566;
 RA Kleerezeem M., Boekhorst J., van Kraanenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Piers M.W.B.J., Stikema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hoffer Groot M.N., Kerhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Siezen R.J.;
 RT "Complete genome sequence of Lactobacillus plantarum WCP51.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).
 CC -!- FUNCTION: Catalyzes the transfer of a methyl group from 5-methyltetrahydrofolate to homocysteine resulting in methionine formation (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-L-glutamate + L-homocysteine = tetrahydropteroyl-L-glutamate + L-methionine.
 CC -!- COFACTOR: Zinc; binds one ion per subunit (By similarity).
 CC -!- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
 CC -!- SIMILARITY: Belongs to the vitamin-B12 independent methionine synthase family.

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CC EMBL; AL93556; CAD63852.1; -.

CC DR HAMAP; MF_00172; -; 1.
 CC DR InterPro; IPR002429; Methionine_synth.
 CC DR Pfam; PF01717; Methionine_Synth_1.
 CC KW Complete proteome; Methionine biosynthesis; Zinc; Repeat; Zinc (BY SIMILARITY).
 FT METAL 650 650 ZINC (BY SIMILARITY).
 FT METAL 652 652 ZINC (BY SIMILARITY).
 FT METAL 735 735 ZINC (BY SIMILARITY).
 SQ SEQUENCE 768 AA; 86432 MW; 477E4CE087ECB24 CRC64;

RESULT 36
 EPBS_MOUSE STANDARD; PRT; 987 AA.
 AC P54761; Q60627;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-B receptor 4 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor MDK-2) (Developmental kinase 2) (Tyrosine kinase MDK-1).
 DE EPHB4 OR MDK2 OR MYK1 OR HTK.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Murinae; Mus.
 OC Mammalia; Eurheria; Rodentia; Sciurognathi; Muridae; Murinae;
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=BALB/C; TISSUE=Kidney;
 MEDLINE=16074837; PubMed=7478528;
 RX Ciolkosz T., Lerch M.M., Ullrich A.;
 RA RT "Cloning, characterization and differential expression of MDK2 and MDK3, two novel receptor tyrosine kinases of the eck/eph family.";
 RT Oncogene 11:2085-2095 (1995).
 RL RN [2].
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Lung;
 RX MEDLINE=94203677; PubMed=8152808;
 RA Ardes A.C., Reid H.H., Zurcher G., Blaschke R.J., Albrecht D.,
 RA Ziemeckla A.;
 RA RT "Expression of two novel eph-related receptor protein tyrosine kinases in mammary gland development and carcinogenesis.";
 RT Oncogene 9:1461-1467 (1994).
 RL CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO EPHRIN-B2.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: DEVELOPING CARDIOVASCULAR SYSTEM.
 CC -!- DEVELOPMENTAL STAGE: ABUNDANT EXPRESSION AT E16.5 IN VARIOUS ORGAN SYSTEMS, INCLUDING THYMUS, HEART, LUNGS AND KIDNEY, WHICH APPEARED TO BE ASSOCIATED WITH CELLS OF ENDOTHELIAL ORIGIN.
 CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -!- SIMILARITY: Belongs to the Tyr Family of protein kinases. Ephrin receptor subfamily.

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CC EMBL; 249084; CAA8909.1; -.

CC DR EMBL; U06834; AAA18591.1; -.

CC DR PIR; I48652; I48652.

CC DR PIR; I48653; I48953.

CC DR HSSP; P23323; 1B4F.

CC DR MGI; MGI:10477; Ephb4.

CC DR InterPro; IPR006209; EGF-like.

CC DR InterPro; IPR01050; Ephrin receptor.

CC DR InterPro; IPR008957; FN_III-like.

DR	InterPro; IPR003961; FN III.	DT	01-NOV-1997 (Rel. 35, Created)
DR	InterPro; IPR003962; ProtIII subd.	DT	01-NOV-1997 (Rel. 35, Last annotation update)
DR	InterPro; IPR009726; Gal-bind like.	DT	01-NOV-1997 (Rel. 35, Last annotation update)
DR	InterPro; IPR007119; Prot_kinase.	DB	Putative short-chain type dehydrogenase/reductase Y4VI (EC 1.-.-.-).
DR	InterPro; IPR001650; SAM.	GN	Y4VI
DR	InterPro; IPR001245; Tyr_pk kinase.	OS	Rhizobium sp. (strain NGR234).
DR	InterPro; IPR008266; Tyr_pk kinase_AS.	OG	Plasmid sym pNCR234a.
DR	Bacteria; Prokaryotobacteria; Rhizobiales;	OC	Bacteria; Prokaryotobacteria; Alphaproteobacteria; Rhizobiales;
DR	Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.	OC	Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
DR	Pfam; PF01404; EPH_1bd; 1.	NCBI_TaxID	394.
DR	Pfam; PF00041; Fn3; 2.	[1]	
DR	Pfam; PF00069; Pkinase; 1.	RN	SEQUENCE FROM N.A.
DR	Pfam; PF00536; SAM; 1.	RX	Medline=97305956; PubMed=9163424;
DR	PRINTS; PRO0014; PTNYPEIII.	RX	Freiberg C.A., Ferret X., Broughton W.J., Rosenthal A.,
DR	PRINTS; PR00109; TYRKINASE.	RA	Broughton R., Bairach A., Freiberg C.A., Ferret X.,
DR	ProDom; PD001495; Ephrin receptor; 1.	RA	"Molecular basis of symbiosis between Rhizobium and legumes."
DR	ProDom; PD000001; Prot_kinase; 1.	RT	Nature 387:394-401(1997).
DR	SMART; SM00061; EPH_1bd; 1.	RL	[2]
DR	SMART; SM00060; Fn3; 2.	RN	SEQUENCE FROM N.A.
DR	SMART; SM00454; SAM; 1.	RX	Medline=98389014; PubMed=8795346;
DR	SMART; SM02181; TYRK_C; 1.	RX	Freiberg C., Ferret X., Broughton W.J., Rosenthal A.,
DR	PROSITE; PS01186; EGF 2; UNKNOWN 1.	RA	"Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	RT	NGR234 using dye terminators and a thermostable 'sequenase'; a
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	RT	beginning."
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	RT	Genome Res. 6:590-600 (1996).
DR	PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.	CC	- - SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
DR	PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.	CC	(SDR) FAMILY. CONTAINS TWO DOMAINS.
DR	KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;	CC	
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
FT SIGNAL	1	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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FT DOMAIN	16	CC	use by non-profit institutions as long as its content is in no way
FT TRANSMEM	539	CC	modified and this statement is not removed. Usage by and for commercial
FT DOMAIN	540	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
FT DOMAIN	561	CC	or send an email to license@isb-sib.ch).
FT DOMAIN	184	CC	
FT DOMAIN	321	CC	
FT DOMAIN	430	CC	
FT DOMAIN	615	CC	
FT DOMAIN	907	CC	
FT SITE	985	CC	
FT NP BIND	621	CC	
FT BINDING	647	CC	
FT ACT_SITE	740	CC	
FT MOD_RES	590	CC	
FT MOD_RES	595	CC	
FT MOD_RES	774	CC	
FT MOD_RES	924	CC	
FT CARBOHYD	203	CC	
FT CARBOHYD	335	CC	
FT CARBOHYD	426	CC	
FT CONFLICT	351	CC	
FT CONFLICT	389	CC	
FT CONFLICT	659	CC	
FT CONFLICT	783	CC	
FT CONFLICT	805	CC	
FT CONFLICT	913	CC	
FT CONFLICT	938	CC	
FT CONFLICT	970	CC	
SQ SEQUENCE	987 AA;	CC	
Query Match	45.1%; Score 37; DB 1; Length 987;	RESULT	39
Best Local Similarity	66.7%; Pred. No. 1.3e+02;	ENRN_BPT7	
Matches	1; Mismatches 2; Indels 0; Gaps 0;	ID	ENRN_BPT7 STANDARD; PRT; 149 AA.
Qy	3 WYASRGIRP 11	AC	P00611; P00611; Standard; PRT; 149 AA.
Db	390 WATRGLRP 398	DT	21-JUL-1986 (Rel. 01, Created)
RESULT 37	Y4VI_RHISN	DT	21-JUL-1986 (Rel. 01, Last sequence update)
ID Y4VI_RHISN	STANDARD;	DB	Endodeoxyribonuclease I (EC 3.1.21.2) (Endonuclease).
AC Q53217;		GN	Bacteriophage T7.
		OS	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;

OC T7-like viruses.
 OC NCBI_TAXID=10760;
 [1] SEQUENCE FROM N.A.
 RP MEDLINE=83241725; PubMed=6864790;
 RX Dunn J.J.; Studier F.W.;
 RA "Complete nucleotide sequence of bacteriophage T7 DNA and the
 RT locations of T7 genetic elements.";
 RT J.Mol.Biol. 166:477-535(1983).
 RL
 RN [2] SEQUENCE OF 17-154 FROM N.A.
 RP STRAIN=New Zealand white;
 RC STRAIN=New Zealand white;
 RX MEDLINE=9057575; PubMed=9337780;
 RA Reno C.; Boykiw R.; Martinez M.L.; Hart D.A.;
 RT "Temporal alterations in mRNA levels for proteinases and inhibitors
 and their potential regulators in the healing media collateral
 ligament.";
 RT Biochem. Biophys. Res. Commun. 252:757-763(1998).
 RL FUNCTION: Complexes with metalloproteinases (such as collagenases)
 CC and irreversibly inactivates them.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TIMP: The activity of TIMP is dependent on the presence of
 CC disulfide bonds (By similarity).
 CC -!- SIMILARITY: Belongs to the TIMP family.
 CC -!- SIMILARITY: Contains 1 NTR domain.
 CC
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 CC
 DR EMBL; AF069713; ARK95005.1; -.
 DR HSSP; P16035; 1BR9;
 DR InterPro; IPI001820; TIMP.
 DR InterPro; IPI00893; TIMP_like.
 DR Pfam; PF00965; TIMP_1.
 DR SMART; SM00206; NTR_1.
 DR PROSITE; PS50189; NTR_1.
 DR PROSITE; PS0028; TIMP_1.
 DR Metalloprotease inhibitor.
 DR NTR.
 FT DOMAIN 1 126
 FT DISULFID 1 72
 FT DISULFID 3 101
 FT DISULFID 13 126
 FT DISULFID 128 175
 FT DISULFID 138 138
 FT DISULFID 146 167
 FT DISULFID 17 17 BY SIMILARITY.
 FT CONFLICT 25 26 BY SIMILARITY.
 FT CONFLICT 58 58 BY SIMILARITY.
 FT CONFLICT 78 78 BY SIMILARITY.
 FT CONFLICT 93 95 BY SIMILARITY.
 FT DISULFID 146 167 BY SIMILARITY.
 FT CONFLICT 17 17 NK -> V (IN REF. 2).
 FT CONFLICT 25 26 NK -> SE (IN REF. 2).
 FT CONFLICT 58 58 Q -> K (IN REF. 2).
 FT CONFLICT 78 78 I -> V (IN REF. 2).
 FT CONFLICT 93 95 NGN -> DGR (IN REF. 2).
 FT CONFLICT 109 109 T -> S (IN REF. 2).
 FT CONFLICT 112 112 A -> S (IN REF. 2).
 FT CONFLICT 131 131 T -> S (IN REF. 2).
 SQ SEQBENCE 194 AA; CRC64;
 Query Match 43.9%; Score 36; DB 1; Length 194;
 Best Local Similarity 58.3%; Pred. No. 31;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 AWYASRGIRPGV 13
 | :| :|| | |
 2 AGYGAKGURKVG 13
 Db
 RESULT 39
 TIM2_RABBIT STANDARD; PRT; 194 AA.
 ID TIM2_RABBIT
 AC Q9TRZ7; O97589;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2004 (Rel. 43, Last sequence update)
 DE Metalloproteinase inhibitor 2 (TIMP-2) (Tissue inhibitor of
 DE metalloproteinases-2).
 GN TIMP2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Leporidae; Oryctolagidae.
 OX NCBI_TAXID=9986;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=9609920; PubMed=8548358;
 RA Wertheimer S.J.; Katz S.I.;
 RT "Molecular Cloning and characterization of rabbit TIMP-2.";
 RL Inflamm. Res. 44:S121-S122(1995).

OC Cricetulus.
 OC NCBI_TaxID=10030;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA SUZUKI Y.;
 RI Submitted (NOV 1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
 CC and irreversibly inactivates them (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: The activity of TIMP2 is dependent on the presence of
 CC disulfide bonds (By similarity).
 CC -!- SIMILARITY: Belongs to the TIMP family.
 CC -!- SIMILARITY: Contains 1 NTR domain.

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DR EMBL; X75924; CAA5528.1; - .
 DR PIR; S38624; S38624.
 DR HSSP; P16035; 1BRA
 DR InterPro; IPR001220; TIMP.
 DR InterPro; IPR008993; TIMP_like.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; NTR; 1.
 DR PROSITE; PS50189; NTR; 1.
 DR PROSITE; PS00088; TIMP; 1.
 KW Metalloprotease inhibitor; Signal.
 FT NON_TER 1 1 BY SIMILARITY.
 FT SIGNAL <1 2 BY SIMILARITY.
 FT CHAIN 3 196 METALLOPROTEINASE INHIBITOR 2 .
 FT DOMAIN 3 128 NTR.
 FT DISULFID 3 74 BY SIMILARITY.
 FT DISULFID 5 103 BY SIMILARITY.
 FT DISULFID 15 128 BY SIMILARITY.
 FT DISULFID 130 177 BY SIMILARITY.
 FT DISULFID 135 140 BY SIMILARITY.
 FT DISULFID 148 169 BY SIMILARITY.
 SQ SEQUENCE 196 AA; 21941 MW; 2ZDAB954AF75381 CRC64;

Query Match 43.9%; Score 36; DB 1; Length 196;
 Best Local Similarity 63.6%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 1 CAWYASRGIRD 11
 Db 177 CAWY--RGAAP 185

Search completed: February 25, 2004, 06:42:59
 Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 25, 2004, 06:40:25 ; Search time 39 Seconds

(without alignments)

121.353 Million cell updates/sec

Title: US-09-700-643A-7

Perfect score: 82

Sequence: 1 CAYVASRGIRPVGRX 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL_25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_fodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Q8y178 anaerobena sp

Q9pgj56 xyella fas

Q8teq6 xyella fas

Q8ta3 streptococc

Q9i2f2 pseudomomas

Q8cwrl streptococc

Q9x4d5 streptococc

Q8fh4 streptomyce

Q89nj5 bradyrhizob

Q9lm51 aracidopisis

Q81713 aracidopisis

Q95n04 sus scrofa

Q9mams aracidopisis

Q8sa86 zea mays (m

Q7upg7 rhodopizell

Q857j2 mycobacteri

Q958m4 versinina de

Q8fs67 corynebacte

Q92ve9 rhizobium m

Q8bul8 mus musculu

Q8nsz0 corynebacte

Q53929 mycobacteri

Q7tzq8 mycobacteri

Q8yni3 anaerobena sp

Q93tw6 stigmatella

Q8bul8

Q8nsz0 corynebacte

Q53929 mycobacteri

Q805e4 perioptothal

ALIGNMENTS

RESULT 1

OBWN12 ID Q8WN12; PRELIMINARY;

AC Q8WN12; PRT; 98 AA.

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DB Preprooprolactin-releasing peptide.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;

OC Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;

OX [1]

RN SEQUENCE FROM N.A.

RP CURLEWIS J.D.; KUSTERS D.H.L.; BARCLAY J.L.; ANDERSON S.T.;

RA "PROLACTIN-RELEASING PEPTIDE (PPR) IN THE EWE: cDNA CLONING, mRNA

RT DISTRIBUTION AND EFFECTS ON PROACTIN SECRETION IN VITRO AND IN

RT VIVO."

RT SUBMITTED (NOV-2001) TO THE EMBL/GEMBANK/DDBJ DATABASES.

RL EMBL; AF450433; AAL47118.1; -

DR SEQUENCE 98 AA; 10513 MW; 2A5331ED62CAA85 CRC64;

SQ [1]

SEQUENCE FROM N.A.

RA CURLEWIS J.D.; KUSTERS D.H.L.; BARCLAY J.L.; ANDERSON S.T.;

RT "PROLACTIN-RELEASING PEPTIDE (PPR) IN THE EWE: cDNA CLONING, mRNA

RT DISTRIBUTION AND EFFECTS ON PROACTIN SECRETION IN VITRO AND IN

RT VIVO."

RT SUBMITTED (NOV-2001) TO THE EMBL/GEMBANK/DDBJ DATABASES.

RL EMBL; AF450433; AAL47118.1; -

DR SEQUENCE 98 AA; 10513 MW; 2A5331ED62CAA85 CRC64;

SQ [1]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	82.9	98	6 OBWN12	Q8wn12 ovis aries
2	58	70.7	117	13 Q9w624	Q9w624 carassius a
3	55.5	420	2	Q9L2Z7	Q931Z7 streptomyce
4	45	54.9	515	2 Q8YUB9	Q8vab9 brevibryozob
5	44	53.7	141	16 Q8PJ39	Q8pj39 xanthomonas
6	44	53.7	146	16 Q8PTT1	Q8pt71 xanthomonas
7	44	53.7	302	16 Q7U207	Q7u207 mycobacteri
8	44	53.7	315	16 P96274	P96274 mycobacteri
9	43	52.4	273	17 Q8ZTH7	Q8zth7 pyrobaculum
10	43	52.4	326	2 Q9E642	Q9f642 stigmatella
11	43	52.4	391	16 Q8B196	Q88196 pseudomonas
12	43	52.4	402	16 Q82IE7	Q82ie7 streptomyce
13	43	52.4	403	5 Q8WRW9	Q8mrw9 drosophila
14	43	52.4	592	16 Q825Q8	Q825Q8 streptomyce
15	43	52.4	1251	5 Q89Q7	Q89q7 drosophila
16	42	51.2	105	16 Q8UG50	Q8ug50 agrobacteri

RESULT 2

Q9W624 ID Q9W624; PRELIMINARY;

AC Q9W624; PRT; 117 AA.

DT 01-OV-1999 (TREMBLrel. 12, Created)

DT 01-OV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

Page 2

RESULT 6		Q8P7T1		PRELIMINARY;		PRT;		146 AA.		
RX	MEDLINE=22709107; PubMed=12788972;	RA	Garnier T., Eiglmeier K., Catus J.-C., Medina N., Mansoor H.,	RA	Pryor M., Dutfoy S., Grondin S., Lacroix C., Monsempé C., Simon S.,	RA	Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,	RA	Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;	
DB	Q8P7T1 ID 108P7T1	PRELIMINARY;	AC	"The complete genome sequence of <i>Mycobacterium bovis</i> .";	RT	Proc. Natl. Acad. Sci. U.S.A. 100: 8777-8782 (2003).	RL	Proc. Natl. Acad. Sci. U.S.A. 100: 8777-8782 (2003).	DR	EMBL; BX248335; CAD3299.1; -.
DB	01-OCT-2002 (TREMBUREL. 22, Last sequence update)	DT	DR	KW	Complete proteome.	DR	Complete proteome.	DR	SEQUENCE 302 AA; 32592 MW; 2A0EF63DA3B50D77 CRC64;	
DB	01-OCT-2002 (TREMBUREL. 22, Last annotation update)	DT	DR	Match	53.7%; Score 44; DB 16; Length 302;	DR	Match	53.7%; Score 44; DB 16; Length 302;	DR	
DB	01-JUN-2003 (TREMBUREL. 24, Last annotation update)	DT	DR	Best Local Similarity 70.0%; Pred. No. 20;	DR	Best Local Similarity 70.0%; Pred. No. 20;	DR	Best Local Similarity 70.0%; Pred. No. 20;	DR	
DB	Protein-export membrane protein.	DR	DR	Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;	DR	Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;	DR	Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;	DR	
DB	Xanthomonas campestris (pv. campestris).	DR	DR	Qy 2 AWYASRGIRP 11	DR	Qy 2 AWYASRGIRP 11	DR	Qy 2 AWYASRGIRP 11	DR	
DB	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.	DR	DR	DN 126 AWYASDLPQ 135	DR	DN 126 AWYASDLPQ 135	DR	DN 126 AWYASDLPQ 135	DR	
DB	NCBI_TaxID=340;	DR	DR	SEQUENCE FROM N.A.	DR	SEQUENCE FROM N.A.	DR	SEQUENCE FROM N.A.	DR	
DB	RN [1]	RC	STRAIN=ANTC 33913 / NCPPB 538;	DR	REMARK 8	DR	REMARK 8	DR	REMARK 8	
DB	RN [2]	RP	MEDLINE=22022445; PubMed=1204217;	DR	P96274	DR	P96274	DR	P96274	
DB	RN [3]	RA	da Silva A.C.R., Farro J.A., Reinach F.C., Farah C.S., Furian L.R.,	DR	ID	DR	ID	AC	ID	
DB	RN [4]	RA	Quaggio R.B., Monteiros-Vitorello C.B., Van Sluys M.A., Almeida N.F.,	DR	P96274	DR	P96274	DR	P96274	
DB	RN [5]	RA	Alves L.M.C., do Amaral A.M., Bertolino C.B., Camargo L.P.A.,	DR	P96274	DR	P96274	DR	P96274	
DB	RN [6]	RA	Camerote G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,	DR	P96274	DR	P96274	DR	P96274	
DB	RN [7]	RA	Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,	DR	AC	AC	AC	AC	AC	
DB	RN [8]	RA	Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,	DR	315 AA.	DR	315 AA.	DR	315 AA.	
DB	RN [9]	RA	Formighieri E.F., Franco M.C., Gregorio C.C., Gruber A.,	DR	PRT;	DR	PRT;	DR	PRT;	
DB	RN [10]	RA	Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,	DR	DT	DT	DT	DT	DT	
DB	RN [11]	RA	Locardi E.C., Machado M.A., Madeira A.M.B.N., Martins-Rossi N.M.,	DR	01-MAR-2002 (TREMBUREL. 03, Created)	DR	01-MAR-2002 (TREMBUREL. 03, Created)	DR	01-MAR-2002 (TREMBUREL. 03, Created)	
DB	RN [12]	RA	Martins E.C., Meidinis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,	DR	DT	DT	DT	DT	DT	
DB	RN [13]	RA	Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,	DR	01-JUN-2003 (TREMBUREL. 24, Last annotation update)	DR	01-JUN-2003 (TREMBUREL. 24, Last annotation update)	DR	01-JUN-2003 (TREMBUREL. 24, Last annotation update)	
DB	RN [14]	RA	Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,	DR	DE	DE	DE	DE	DE	
DB	RN [15]	RA	Spinola L.A.F., Tabita M.A., Tamura R.E., Teixeira B.C.,	DR	Hypothetical protein Rv0428C.	DR	Hypothetical protein Rv0428C.	DR	Hypothetical protein Rv0428C.	
DB	RN [16]	RA	Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,	DR	RV0428C OR MT0443 OR MT22G10.25C.	DR	RV0428C OR MT0443 OR MT22G10.25C.	DR	RV0428C OR MT0443 OR MT22G10.25C.	
DB	RN [17]	RA	Setubal J.C., Kitajima J.P.;	DR	OS	OS	OS	OS	OS	
DB	RN [18]	RA	SEQUENCE OF two xanthomonas pathogens with differing host specificities";	DR	Mycobacterium tuberculosis.	DR	Mycobacterium tuberculosis.	DR	Mycobacterium tuberculosis.	
DB	RN [19]	RA	Nature 417:459-463 (2002).	DR	RX MEDLINE=98295987; PubMed=9634230;	DR	RX MEDLINE=98295987; PubMed=9634230;	DR	RX MEDLINE=98295987; PubMed=9634230;	
DB	RN [20]	RA	EMBL; AE012364; AVA41803.1; -.	DR	RA Cole S.T., Brosh R., Parkhill J., Garnier T., Churcher C., Harris D.,	DR	RA Cole S.T., Brosh R., Parkhill J., Garnier T., Churcher C., Harris D.,	DR	RA Cole S.T., Brosh R., Parkhill J., Garnier T., Churcher C., Harris D.,	
DB	RN [21]	RA	GO: GO:0016021; C:integral to membrane; IEA.	DR	RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekla P.,	DR	RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekla P.,	DR	RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekla P.,	
DB	RN [22]	RA	GO: GO:0015450; P:protein in translocone; ACTIN.	DR	RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,	DR	RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,	DR	RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,	
DB	RN [23]	RA	GO: GO:0009306; P:protein secretion; IEA.	DR	RA Davies R., Devlin P., Feltwell T., Gentles S., Hamlin N., Holroyd S.,	DR	RA Davies R., Devlin P., Feltwell T., Gentles S., Hamlin N., Holroyd S.,	DR	RA Davies R., Devlin P., Feltwell T., Gentles S., Hamlin N., Holroyd S.,	
DB	RN [24]	RA	GO: GO:0009306; P:protein secretion; IEA.	DR	RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,	DR	RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,	DR	RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,	
DB	RN [25]	RA	InterPro IPR004692; SEC61.	DR	RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,	DR	RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,	DR	RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,	
DB	RN [26]	RA	Pfam PF03840; SEC61_1.	DR	RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,	DR	RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,	DR	RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,	
DB	RN [27]	RA	PRINTS PR01651; SEC61EXPORT.	DR	RA Sulston J.B., Taylor K., Whithead S., Barrel B.G.;	DR	RA Sulston J.B., Taylor K., Whithead S., Barrel B.G.;	DR	RA Sulston J.B., Taylor K., Whithead S., Barrel B.G.;	
DB	RN [28]	RA	Complete proteome.	DR	RT "Deciphering the biology of <i>Mycobacterium tuberculosis</i> from the complete genome sequence."	DR	RT "Deciphering the biology of <i>Mycobacterium tuberculosis</i> from the complete genome sequence."	DR	RT "Deciphering the biology of <i>Mycobacterium tuberculosis</i> from the complete genome sequence."	
DB	RN [29]	RA	SEQUENCE 146 AA; 14481 MW; 503AABAD982C04CB CRC64;	DR	Nature 393:537-544 (1998).	DR	Nature 393:537-544 (1998).	DR	Nature 393:537-544 (1998).	
DB	RN [30]	RA	RT RT SEQUENCE FROM N.A.	DR	RN RN SEQUENCE FROM N.A.	DR	RN RN SEQUENCE FROM N.A.	DR	RN RN SEQUENCE FROM N.A.	
DB	RN [31]	RA	RT RT STRAIN=CDC 1551 / Oshkosh;	DR	RC RC STRAIN=CDC 1551 / Oshkosh;	DR	RC RC STRAIN=CDC 1551 / Oshkosh;	DR	RC RC STRAIN=CDC 1551 / Oshkosh;	
DB	RN [32]	RA	RT RT Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,	DR	RA RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickie E., Kolonay J.P., Nelson W.C., Unayam L.A., Errolsaya M., Salberg S.L., Bishai W.;	DR	RA RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickie E., Kolonay J.P., Nelson W.C., Unayam L.A., Errolsaya M., Salberg S.L., Bishai W.;	DR	RA RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickie E., Kolonay J.P., Nelson W.C., Unayam L.A., Errolsaya M., Salberg S.L., Bishai W.;	
DB	RN [33]	RA	RT RT "Whole genome comparison of <i>Mycobacterium tuberculosis</i> clinical and laboratory strains."	DR	RT RT Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.	DR	RT RT Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.	DR	RT RT Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.	
DB	RN [34]	RA	RT RT DR EMBL; Z84724; CAB06368.1; ALT_INIT.	DR	RA RA DR EMBL; Z84724; CAB06368.1; ALT_INIT.	DR	RA RA DR EMBL; Z84724; CAB06368.1; ALT_INIT.	DR	RA RA DR EMBL; Z84724; CAB06368.1; ALT_INIT.	
DB	RN [35]	RA	RT RT DR PIR; B70631; B70631.	DR	RA RA DR PIR; B70631; B70631.	DR	RA RA DR PIR; B70631; B70631.	DR	RA RA DR PIR; B70631; B70631.	
DB	RN [36]	RA	RT RT DR TIGR; MT0443; MT0443.	DR	RA RA DR TIGR; MT0443; MT0443.	DR	RA RA DR TIGR; MT0443; MT0443.	DR	RA RA DR TIGR; MT0443; MT0443.	
DB	RN [37]	RA	RT RT DR Tuberculise; Rv0428C; -.	DR	RA RA DR Tuberculise; Rv0428C; -.	DR	RA RA DR Tuberculise; Rv0428C; -.	DR	RA RA DR Tuberculise; Rv0428C; -.	
DB	RN [38]	RA	RT RT KW Hypothetical protein Rv0428C.	DR	RA RA KW Hypothetical protein Rv0428C.	DR	RA RA KW Hypothetical protein Rv0428C.	DR	RA RA KW Hypothetical protein Rv0428C.	
DB	RN [39]	RA	RT RT SQ SEQUENCE 315 AA; 34099 MW; 3BBE6399C4C0C7B7 CRC64;	DR	RA RA SQ SEQUENCE 315 AA; 34099 MW; 3BBE6399C4C0C7B7 CRC64;	DR	RA RA SQ SEQUENCE 315 AA; 34099 MW; 3BBE6399C4C0C7B7 CRC64;	DR	RA RA SQ SEQUENCE 315 AA; 34099 MW; 3BBE6399C4C0C7B7 CRC64;	
DB	RN [40]	RA	RT RT SEQUENCE FROM N.A.	DR	RA RA SEQUENCE FROM N.A.	DR	RA RA SEQUENCE FROM N.A.	DR	RA RA SEQUENCE FROM N.A.	
DB	RN [41]	RA	RT RT RP	DR	RA RA RP	DR	RA RA RP	DR	RA RA RP	

Db	139 AWYASRDLOP 148	Qy	2 AWYASRGIRP 11
		Db	: : : : 79 SWLASRGIKP 88
RESULT 9			
Q8ZTH7	PRELIMINARY;	PRT;	273 AA.
ID Q8ZTH7;			
AC 01-MAR-2002 (TREMBLrel. 20, Created)			
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE Morphine 6-dehydrogenase, conjectural.			
GN PAE247.			
OS Pyrococcus aerophilum.			
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;			
OC Thermoproteaceae; Pyrococcaceae.			
OX NCBI_TaxID=13773;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=JM2 / ATCC 51768 / DSM 7523;			
RX MEDLINE=1664397; PubMed=11792863;			
RA Fitch-Gibson S.T., Ladner H., Kim U.-J., Stettler K.O., Simon M.I., Miller J.H.;			
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrococcus aerophilum.", Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).			
RL EMBL; AE009920; AL64784.1; -.			
DR IPR001305; Aldo/ket_red.			
PFam: PF00248; aldo_ket_red_1.			
PRINTS; PR00069; ALDKEFDTAE.			
DR PRO0088; Aldo/ket_red_1.			
KW Complete proteome; RT			
SEQUENCE 273 AA; 30203 MW; 3F9D1208FB10DF7F CRC64;			
Query Match 52.4%; Score 43; DB 17; Length 273; Best Local Similarity 54.5%; Pred. No. 27;			
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;			
Qy 2 AWYASRGIRPV 12			
Db 228 AWYVVRGVVPI 238			
RESULT 10			
Q9F642	PRELIMINARY;	PRT;	326 AA.
ID Q9F642;			
AC 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
MXCA.			
OS Stigmatella aurantiaca.			
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterinae; Cystobacteraceae; Stigmatellidae.			
NCBI_TaxID=41;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=SG_a15;			
DR MEDLINE=0495524; PubMed=11029592;			
RA Silakowski B., Kunze B., Nordsiak G., Blocker H., Hofle G., Muller R.;			
RT "The myxochelin iron transport regulon of the myxobacterium Stigmatella aurantiaca SG_a15.", Eur. J. Biochem. 267:6476-6485 (2000).			
RL EMBL; AF299336; AAC31124.1; -.			
DR InterPro: IPR001395; Aldo/ket_red.			
DR PF00248; aldo_ket_red_1.			
DR PRO0088; Aldo/ket_red_1.			
SQ SEQUENCE 326 AA; 35096 MW;			
Query Match 52.4%; Score 43; DB 2; Length 326; Best Local Similarity 70.0%; Pred. No. 32;			
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;			
RESULT 11			
Q8816	PRELIMINARY;	PRT;	391 AA.
ID Q8816;			
AC Q88196;			
DT 01-JUN-2003 (TREMBLrel. 24, Created)			
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DE Conserved hypothetical protein.			
GN PP3103.			
OS Pseudomonas putida (strain KT2440).			
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.			
OC NCBI_TaxID=160488;			
OX [1] -			
RN RP SEQUENCE FROM N.A.			
RX MEDLINE=22423160; PubMed=12534463;			
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Dodson R.J., Hilbert H., Nelson K.E., Weinert C., Paulsen I.T., Daugherty S., Kolonay J., Brinkac L., Beanan M., DeBoy R.T., Peterson J., Khouri H., Hance I., Madupu R., Nelson W., White O., Holzapple E., Scanlan D., Tran K., Moazzez A., Chris Lee P., Holzapfle B., Rizzoli M., Lee K., Kosack D., Moestel D., Wedler H., Lauber J., Stiepanik D., Hoheisel J., Straetz M., Haim S., Kiewitz C., Eisen J., Timmis K.N., Dueberhoft A., Tuernier B., Fraser C.M., TIGR PP3103; -.			
RA "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440.", Environ. Microbiol. 4:799-808 (2002).			
DR EMBL; AE016785; AAN68711.1; -.			
RT "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440.", Environ. Microbiol. 4:799-808 (2002).			
RL SQ SEQUENCE 391 AA; 42389 MW;			
DR XSEA OR SAV3211.			
RT Query Match 52.4%; Score 43; DB 16; Length 391; Best Local Similarity 50.0%; Pred. No. 39; Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;			
Qy 2 AWYASRGIRVG 13			
Db 85 AWFAEDGLKEDAG 96			
RESULT 12			
Q821E7	PRELIMINARY;	PRT;	402 AA.
ID Q821E7;			
AC 0821E7;			
DT 01-JUN-2003 (TREMBLrel. 24, Created)			
DT 01-OCT-2003 (TREMBLrel. 24, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 24, Last annotation update)			
DB Putative exoribonuclease large subunit.			
GN XSEA OR SAV3211.			
OS Streptomyces avermitilis.			
OC Bacteria; Actinobacteria; Streptomyctaceae; Streptomyces.			
OC NCBI_TaxID=33993;			
RN RN SEQUENCE FROM N.A.			
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;			
RX MEDLINE=21477403; PubMed=11572948;			
RA Omura S., Ikeda H., Ishii-Kawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Ono T., Kikuchi H., Shiba T., Hattori M., "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites"; Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).			
RT [2]			
RP SEQUENCE FROM N.A.			

RC STRAIN MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
RR MEDLINE=2268300; PubMed=1692362;	DB Strain=MA-4680; Productivity=1,4-alpha-glucan branching enzyme.
RA Tkeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakai Y., Hattori M., Omura S.;	GN SAV7399.
RA "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.",	OS Streptomyces avermitilis.
RT Bacterium; Actinobacteria; Actinomycetales;	OC Streptomyctaceae; Streptomyces.
RI Nat. Biotechnol. 21:526-531 (2003).	OC NCBI_TaxID=33903;
DR EMBL; AP005034; BAC7091.1;	OX [1].
DR GO; GO:0009318; C:exodeoxyribonuclease VII complex; IEA.	RP SEQUENCE FROM N.A.
DR GO; GO:0008555; F:exodeoxyribonuclease VII activity; IEA.	RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
DR GO; GO:003576; F:nucleic acid binding; IEA.	RX MEDLINE=1477403; PubMed=11572948;
DR GO; GO:0006108; P:DNA catabolism; IEA.	RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shirose M., Takahashi Y., Horikawa H., Nakazawa H., Osoneo T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.
DR InterPro; IPR003753; Exonuc VII_L.	RA "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites";
DR InterPro; IPR004365; tRNA_anti_L.	RT RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).
DR PFam; PF02601; Exonuc_VII_L1.	RL [2].
DR TIGRFAMS; TIGR00237; xSEA_1.	RL SEQUENCE FROM N.A.
KW Complete proteome.	RN STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
SC SEQUENCE 402 AA; 43844 MW; 863AB19C4C8F4A07 CRC64;	RC MEDLINE=2268306; PubMed=12892562;
Qy Query Match 52.4%; Score 43; DB 16; Length 402; Best Local Similarity 47.4%; Pred. No. 40; Matches 9; Conservative 1; Mismatches 1; Indels 8; Gaps 1;	RX RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sasaki Y., Hattori M., Omura S.;
Db 3 WYASRG-----IRPGV 13	RA "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Db 91 WYAPRGQISLRRAEIRPIG 109	RT RT RL Nat. Biotechnol. 21:526-531 (2003).
RESULT 13 Q8MRW9 PRELIMINARY; PRT; 403 AA.	RL EMBL; AP005034; BAC7511.1;
Q8MRW9 ID Q8MRW9	DR GO; GO:0003844; F:1,4-alpha-glucan branching enzyme activity; IEA.
AC Q8MRW9	DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DT 01-OCT-2002 (TREMBLrel. 22, Created)	DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)	DR InterPro; IPRO06047; Alpha_amyl_cat.
DE SD16815P	DR InterPro; IPRO06559; Alpha_amyl_cat_sub.
GN CG3161.9 OR CG2122 OR CG2131 OR CG13236.	DR InterPro; IPRO06407; GlyB.
OS Drosophila melanogaster (fruit fly).	DR InterPro; IPRO04153; Glyco_hydro_13N.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Neoceridae; Drosophilidae; Drosophila.	DR Pfam; PF00128; alpha-amylase_1.
OC Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.	DR SMART; SM00632; Amyl_1.
RL EMBL:AY119222; AACM51082.1;	DR TIGRFAMS; TIGR01515; branching_enzym; 1.
DR FBn00051619; CG3161.9.	KW Complete proteome.
DR InterPro; IPR000884; TSP1.	SQ SEQUENCE 592 AA; 66805 MW; 3A7355BE0360BC51 CRC64;
DR PROSITE; PS00092; TSP1; 2.	Query Match 52.4%; Score 43; DB 16; Length 592; Best Local Similarity 72.7%; Pred. No. 61; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
SQ SEQUENCE 403 AA; 45343 MW; 1040B5951B8380C9 CRC64;	Qy 2 AWYASRGIRPV 12
Qy 1 CAMYASSRGIRPGV 13	Db 103 AWYASRGIRPV 113
Db 322 CWWYGSR-RPG 332	RESULT 14 Q9V967 PRELIMINARY; PRT; 1353 AA.
Q9V967 ID Q9V967 PRELIMINARY; PRT; 1353 AA.	RR SEQUENCE FROM N.A.
AC Q9V967	RC STRAIN=Berkeley;
DT 01-MAY-2000 (TREMBLrel. 13, Created)	RC MEDLINE=0196006; PubMed=10731122;
DT 01-OCT-2003 (TREMBLrel. 22, Last sequence update)	RX Adams M.D., Celiker S.B., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.F., NCBI_TaxID=7227;
DB CG31619 OR CG2122 OR CG2131 OR CG13236.	OX [1].
OS Drosophila melanogaster (fruit fly).	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Drosophila; Drosophilidae; Drosophila.
OC Ephydriidea; Drosophilidae; Drosophila.	OC NCBI_TaxID=7227;
OX [1].	RN

Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen"; Nature 406:959-964 (2000); DR PIR; GS3400; G83400; -.

RA GO:0016021; C:internal to membrane; IEA.

GO; GO:0015450; F:protein translocase; activity; IEA.

GO; GO:0009306; P:protein secretion; IEA.

InterPro; IPR004632; SecG.

PFAM; PF03944; SecG_1.

PRINTS; PRO1651; SECGEPORT.

Complete Proteome; PRO1651; SECGEPORT.

KW SEQUENCE 132 AA; 13605 MW; 676040062CC77808 CRC64;

Query Match Score 42; DB 16; Length 132; Best Local Similarity 61.5%; Pred. No. 18; Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AWYASRGIRPVGR 14
Dbs 70 AWYASRGHHSVAQ 82

RESULT 20

Q88TA3 Q8RTA3 PRELIMINARY; PRT; 223 AA.

Q8RTA3; 01-JUN-2002 (TREMBLrel. 21; Created) 01-JUN-2002 (TREMBLrel. 21; Last sequence update) 01-MAR-2003 (TREMBLrel. 23; Last annotation update)

DT DE LiCD2 (Fragment).

DS Streptococcus pneumoniae.

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

NCBI_TAXID=1313;

RN STRAIN=WB44_1;

RC Weisser J.N.; Bae D.H.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

RA EMLB; AF467731; ABL7732_1; -.

DR InterPro; IPR007074; LicD.

DR Frame; PF04991; LicD_1.

DR NON_TER 223 223

SQ SEQUENCE 223 AA; 26566 MW; COFC9A3A7AC75384 CRC64;

Query Match Score 42; DB 2; Length 223; Best Local Similarity 54.5%; Pred. No. 32; Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAYWASRGIRP 11
Dbs 166 CSWYALRFVNP 176

RESULT 21

O9I2F2 O9I2F2 PRELIMINARY; PRT; 250 AA.

AC 01-MAR-2001 (TREMBLrel. 16; Created) 01-MAR-2001 (TREMBLrel. 16; Last sequence update) 01-OCT-2003 (TREMBLrel. 25; Last annotation update)

DE Hypothetical protein PA1952.

JN PA1952.

DS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

NCBI_TAXID=287;

RN SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=WB44_1;

RC Weisser J.N.; Bae D.H.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

RA EMLB; AF467731; ABL7732_1; -.

DR InterPro; IPR007074; LicD.

DR Frame; PF04991; LicD_1.

DR NON_TER 223 223

SQ SEQUENCE 223 AA; 26566 MW; COFC9A3A7AC75384 CRC64;

Query Match Score 42; DB 16; Length 250; Best Local Similarity 53.8%; Pred. No. 36; Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAYWASRGIRPGV 13
Dbs 237 CAVEQLRRAIRPSG 249

RESULT 22

O8CWR1 O8CWR1 PRELIMINARY; PRT; 269 AA.

AC 08CWR1; 01-MAR-2003 (TREMBLrel. 23; Created) 01-MAR-2003 (TREMBLrel. 23; Last sequence update) 01-JUN-2003 (TREMBLrel. 24; Last annotation update)

DE LiCD protein.

GN LICD2 OR SPR1152.

OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

OC NCBI_TaxID=171101;

OX RN

SEQUENCE FROM N.A.

MDLINE=21439245; PubMed=11544234;

RA Hoskins J., Albion W.E. Jr., Blaszczyk L.C., Burgeit S., Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lee J.J., Matsushima P., McAheren S.M., McHenney M., McLeaster K., Mundt C.W., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.M., Winkler M.E., Yang Y., Young-Heliodoro M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L., Zook J.

RA "Genome of the bacterium Streptococcus pneumoniae strain R6.";

RA RL J. Bacteriol. 183:5709-5717 (2001).

RA DR PIR; A95148; A95148.

RA DR PIR; GS8015; G98015.

RA DR InterPro; IPR07074; LicD.

RA DR Pfam; PF04991; LicD_1.

RA KW Complete proteome.

SQ SEQUENCE 32100 MW; 31A152DFAA480A10 CRC64;

Query Match Score 42; DB 16; Length 269; Best Local Similarity 54.5%; Pred. No. 39; Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAYWASRGIRP 11
Dbs 166 CSWYALRFVNP 176

RESULT 23

O9X4D5 O9X4D5 PRELIMINARY; PRT; 269 AA.

AC 01-NOV-1999 (TREMBLrel. 12; Last sequence update) 01-NOV-1999 (TREMBLrel. 12; Last sequence update) 01-OCT-2003 (TREMBLrel. 25; Last annotation update)

DR LICD2.

DN LICD2 OR SP1274.

Stover K.C., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Gooley L., Tolentino E., Wessbrock-Wadman S., Yuan Y., Garber R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spener D.H., Wong C.K.-S., Wu J., Paulsen T.M.,

OS Streptococcus pneumoniae.	RX MEDLINE=22608306; PubMed=12692562;
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	RA Ikeda H.; Ishikawa J.; Hamamoto A.; Shinose M.; Kikuchi H.; Shiba T.,
OC Streptococcus.	RA Sakai Y.; Hattori M.; Omura S.;
OX NCBI_TaxID=1313;	RT "Complete genome sequence and comparative analysis of the industrial
RN [1]	microorganism Streptococcus avermitilis.";
RP SEQUENCE FROM N.A.	RT
RC STRAIN=R6X;	RL Nat.
RX MEDLINE=9917023; PubMed=10200966;	DR EMBL; AP005038; BAC71990.1;
RA Zhang J.R.; Idaanpa-Heikkila I.; Fischer W.; Tuomanen E.I.;	GO; GO:0008080; F:N-acetyltransferase activity; IER.
RT "Pneumococcal licD2 gene is involved in phosphorylcholine	InterPro; IPR000182; GCN5acyltransferase.
RT metabolism.";	Pfam; PF00583; Acetyltransferase_1.
RT Mol. Microbiol. 31:1477-1488 (1999).	KW Hypothetical protein; Complete proteome.
RN [2]	SQ SEQUENCE 288 AA; 31063 MW; 275CA1541D7B3 CRC64;
RP SEQUENCE FROM N.A.	Query Match Score 42; DB 16; Length 288;
RC STRAIN=ATCC BAA-334 / TIGR4; PubMed=11463916;	Best Local Similarity 58.3%; Pred. No 42;
RX MEDLINE=21357209; PubMed=11463916;	Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
RA Tettelin H.; Nelson K.E.; Paulsen I.T.; Eisen J.A.; Read T.D.,	AC Q89N5 PRELIMINARY; PRT; 289 AA.
RA Peterson D.H.; Haft D.H.; Dodson R.J.,	DT 01-JUN-2003 (TREMBLrel. 24; Created)
RA Durkin A.S.; Gwin M.; Kolonay J.F.; Nelson W.C.; Peterson J.D.,	DT 01-JUN-2003 (TREMBLrel. 24; Last sequence update)
RA Umayam L.A.; White O.; Salzberg S.L.; Lewis M.R.; Radune D.,	DT 01-JUN-2003 (TREMBLrel. 24; Last annotation update)
RA Holtzapfel B.; Khouri H.; Wolf A.M.; Utterback T.R.; Hansen C.L.,	DE Bir3843 protein.
RA McDonald L.A.; Feldblyum T.V.; Angiuoli S.; Dickinson T.; Hickey E.K.,	GN BLR3843
RA Holt I.E.; Loftus B.J.; Yang F.; Smith H.O.; Venter J.C.,	OS Bradyrhizobium japonicum.
RA Dougherty B.A.; Morrison D.A.; Hollingshead S.K.; Fraser C.M.,	OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
RT "Complete genome sequence of a virulent isolate of Streptococcus	OC Bradyrhizobiaceae; Bradyrhizobium.
RT pneumoniae";	OX NCBI_TaxID=375;
RL SCIENCE 293:498-506(2001)	RN [1]
DR AF10539; ADD31094.1; -.	RP SEQUENCE FROM N.A.
DR EMBL; AF10539; ADD31094.1; -.	RC STRAIN=USDA 110;
DR PIR; A95148; A95148.	RX MEDLINE=2481998; PubMed=125997275;
DR PIR; G98015; G98015.	RA Kaneko T.; Nakamura Y.; Sato S.; Minamisawa K.; Uchiimi T.,
DR TIGR; SP1274; -.	RA Sasamoto S.; Watanabe A.; Tiede K.; Iriuchishi M.; Kawashima K.,
DR InterPro; IPR007074; LicD.	RA Kohara M.; Matsutomo M.; Shimpo S.; Tsuruoka H.; Wada T.; Yanada M.,
DR Pfam; PF04991; LicD; 1.	RA Tabata S.;
DR Complete proteome; NCBI_TaxID=375;	RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RW SEQUENCE 269 AA; 32100 MW; 31A152DFAR480A10 CRC64;	RT Bradyrhizobium japonicum USDA110.";
SQ Query Match Score 42; DB 16; Length 269;	RT DNA Res. 9:189-197 (2002).
Best Local Similarity 54.5%; Pred. No 39;	DR EMBL; AP005949; BAC49108.1; -.
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	KW Complete proteome; 30D4B03A4ED8A3FD CRC64;
QY 1 CAWYASRGIRPV 11	SQ SEQUENCE 289 AA; 32151 MW; 30D4B03A4ED8A3FD CRC64;
Db 166 CSWYALRFVNP 176	Query Match Score 42; DB 16; Length 289;
OS Streptomyces avermitilis.	Best Local Similarity 60.0%; Pred. No 42;
OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;	Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OC Streptomyceinae; Streptomyctaceae; Streptomyces.	Qy 3 WYASRGIRPV 12
OX NCBI_TaxID=33903;	Db 197 WYASRGIVVPI 206
RN [1]	RESULT 26
RP SEQUENCE FROM N.A.	Q9LM51 PRELIMINARY; PRT; 487 AA.
RC STRAIN=MA-6680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;	AC Q9LM51; PRELIMINARY;
RX MEDLINE=21477403; PubMed=11572948;	AC Q9LM51; PRELIMINARY;
RA Omura S.; Ikeda H.; Ishikawa J.; Hamamoto A.; Takahashi C.,	DT 01-OCT-2000 (TREMBLrel. 15; Created)
RA Shinose M.; Takahashi Y.; Horikawa H.; Nakazawa H.; Osono T.,	DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)
RA Kikuchi H.; Shiba T.; Sakai Y.; Hattori M.;	DE F2E2.15.
RT "Genome sequence of an industrial microorganism Streptomyces	OS Arabidopsis thaliana (Mouse-ear cress).
RT avermitilis: deducing the ability of producing secondary	OC Spermatophyta; Magnoliophyta; Embryophytes; Tracheophyta;
RT metabolites";	OC Eudicots; core eudicots; rosids;
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).	OC eurids II; Brassicales; Brassicaceae; Arabidopsis.
RN [2]	OX NCBI_TaxID=375;
RP SEQUENCE FROM N.A.	RN [1]
RX STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;	
RC	

RESULT 29	[3]	RN	SEQUENCE FROM N.A.
Q9MAB8 PRELIMINARY;	PRT; 656 AA.	RP	STRAIN=ev. B73;
ID Q9MAB8		RC	EMBL; Young S., Kovchoh S., Messing J.;
AC Q9MAB8;		RA	Lilaca V., Linton E.W., Young S., Kovchoh S., Messing J.;
DT 01-OCT-2000 (TREMBLrel. 15, Created)		RL	Submitted (JAN-2002) to the EMBL/GenBank/DDJB databases.
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)		DR	EMBL; AF466616; AAL76006; 1; -.
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		DR	InterPro; IPR007321; Transpose 28; 1.
DB T25K16_6.		DR	PFam; PF04135; Transpose 28; 1.
OS Arabidopsis thaliana (Mouse-ear cress);		SQ	SEQUENCE 918 AA; 103639 MW; 11F4E95C34039495 CRC64;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
euroids II; Brassicales; Brassicaceae; Arabidopsis.			
NCBI_TAXID=3702;			
RN [1]			
RP	Query Match 51.2%; Score 42; DB 10; Length 918;		
RA Dunn P., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altieri H., Bei Q., Chin C., Chiu J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federer Spiel N.A., Theologis A., Ecker J.R.;	Best Local Similarity 87.5%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
RA "Genomic sequence for Arabidopsis thaliana BAC T25K16 from chromosome 1." Submitted (JAN-2000) to the EMBL/GenBank/DDJB databases.	Query Match 51.2%; Score 42; DB 10; Length 918;	QY	1 CAYTASRG 8
RL CC	Best Local Similarity 87.5%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Db	836 CAYTASRG 843
CC -I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).	RESULT 31		
CC -I- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.	Q7UBG7 PRELIMINARY;		
CC -I- SIMILARITY: GO:00005634; C:nucleus; IEA.	ID Q7UBG7		
DR GO:00005677; F:DNA binding; IEA.	AC 01-OCT-2003 (TREMBLrel. 25, Created)		
DR InterPro; IPR001005; Myb DNA binding.	DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)		
DR InterPro; IPR006447; Myb SHAOKYF.	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DR InterPro; IPR001045; Myb DNA-binding; 1.			
DR SMART; SM0017; SAN7; 1.			
DR TIGRFAMs; TIGR01557; myb SHAOKYF; 1.			
DR PROSITE; PS50090; MYB_3_1.			
DR PROSITE; PS50090; MYB_3_1.			
KW DNA-binding; Nuclear protein.			
KW SEQUENCE 656 AA; 71794 MW; E3D08CF31F739A2E CRC64;			
SQ			
Query Match 51.2%; Score 42; DB 10; Length 656;	Query Match 51.2%; Score 42; DB 16; Length 1120;		
Best Local Similarity 63.6%; Pred. No. 1e+02; Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	Best Local Similarity 70.0%; Pred. No. 1.8e+02; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;		
QY 2 ANYASRGIRP 12	QY 2 AWYASRGIRP 11		
Db 368 AWYASRGIRP 378	Db 206 AWYASRGIRP 215		
RESULT 30			
Q8SA86 PRELIMINARY;	PRT; 918 AA.		
ID Q8SA86;			
AC Q8SA86;			
DT 01-JUN-2002 (TREMBLrel. 21, Created)	RESULT 32		
DE Putative retrotransposon protein.	Q857J2 PRELIMINARY;		
GN 2195D10_18.	ID Q857J2		
OS Zea mays (Maize)	AC Q857J2		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	DT 01-JUN-2003 (TREMBLrel. 24, Created)		
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)		
PACCD clade; Panicoideae; Andropogoneae; Zea.	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
NCBI_TAXID=4577;	DB Gp30.		
RN [1]	OS Mycobacteriophage Bx22.		
RP SEQUENCE FROM N.A.	OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.		
RC SPEAIN=ev. B73;	OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.		
RA Ramakrishna W., Emberton J., SanMiguel P., Bennetzen J.; Submitted (JAN-2002) to the EMBL/GenBank/DDJB databases.	OX NCBI_TAXID=205870;		
RN [2]	RN [1] SEQUENCE FROM N.A.		
RC STRAIN=ev. B73;	RP SEQUENCE FROM N.A.		
RA Deobley J.; Submitted (JAN-2002) to the EMBL/GenBank/DDJB databases.	RX MEDLINE=22592660; PubMed=12705866;		
RA	RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikayan T., Wadsworth C., Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R., Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S., Krikorov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,		

RA	Hatfull G.F.;	"Origins of highly mosaic mycobacteriophage genomes."		
RT	Cell 113:171-182(2003);			
RL	EMBL; AY-19332; AA_1784..1;			
DR	PF00448; aldo_ket_red; 1.			
DR	PF00069; ALDOKETOREDUCTASE;			
PRINTS	PD000288; Aldo/ket_red; 1.			
PRODOM	PS000798; ALDOKETO_REDUCtASE_1;			
DR	PS00022; ALDOKETO_REDUCtASE_2;			
DR	PS00063; ALDOKETO_REDUCtASE_3;			
KW	Complete proteome.			
SEQUENCE	246 AA; 9BB9A6402F9D27DD CRC64;			
Qy	2 AWYASRGIRPVGR 14			
Db	88 AWWIRRNTPVYGK 100			
RESULT 33				
Q858w4	PRELIMINARY;	PRT;	151 AA.	
AC	Q858w4;			
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Endonuclease.			
OS	Versinia pestis phage phiAl122.			
OC	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;			
OC	T-like viruses.			
OX	NCBI_TaxID=227720;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Garcia E., Elliott J.M., Ramankulov E., Chain P.S., Chu M.C.,			
RA	Molineux I.J.;			
RT	"The genome sequence of Yersinia pestis bacteriophage PhiAl122 reveals an intimate history with the coliphage T3."			
RT	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY247822; AA B020511..1; -			
DR	GO:000833; P:Deoxyribonuclease IV (phage-T4-induced)	act.	.	IEA.
DR	GO:0004519; P:Endonuclease activity; IEA.			
DR	GO:0015074; P:DNA integration; IEA.			
DR	GO:0016332; P:Viral life cycle; IEA.			
DR	InterPro; IPR008022; Phage_endo_I.			
DR	Pfam; PF03367; Phage_endo_I..1.			
KW	Endonuclease.			
SEQUENCE	151 AA; 17402 MW; 1EA8D071D41BB979 CRC64;			
Qy	Query Match 50.0%; Score 41, DB 9; Length 151;			
Db	Best Local Similarity 80.0%; Pred. No. 31;			
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Last annotation update)			
Qy	4 YASRGIRPYG 13			
Db	5 YAARSTIRKG 14			
RESULT 34				
Q8F567	PRELIMINARY;	PRT;	246 AA.	
AC	Q8F567;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-OCT-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-DEC-2003 (TREMBLrel. 25, Last annotation update)			
DE	Putative oxidoreductase.			
CN	Q8F537.			
OS	Corynebacterium efficiens.			
OC	Bacteria; Actinobacteria; Actinomycetales;			
CC	Corynebacteriaceae; Corynebacterium.			
OX	NCBI_TaxID=152794;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=IS-314 / AJ_12310 / DSM 44549 / JCM 11189;			
RA	Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,			
RA	Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,			
RA	Usuda Y., Sugimoto S.;			
RT	"The entire genomic sequence of Corynebacterium efficiens IS-314."			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AP009215; BAC17347..1;			
DR	InterPro; IPR01395; Aldo/ket_red.			
DR	PF00448; aldo_ket_red; 1.			
PRINTS	PS00069; ALDOKETOREDUCTASE;			
PRODOM	PD000288; Aldo/ket_red; 1.			
DR	PS000798; ALDOKETO_REDUCtASE_1;			
DR	PS00022; ALDOKETO_REDUCtASE_2;			
DR	PS00063; ALDOKETO_REDUCtASE_3;			
KW	Complete proteome.			
SEQUENCE	246 AA; 27766 MW; 9BB9A6402F9D27DD CRC64;			
Qy	2 AWYASRGIRPVGR 14			
Db	187 AWHHARGIVPPIR 199			
RESULT 35				
Q92VE9	PRELIMINARY;	PRT;	256 AA.	
ID	Q92VE9;			
AC	Q92VE9;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Hypothetical protein RB0757.			
GN	GNB57 OR SMB21253.			
OS	Rhizobium meliloti (Sinorhizobium meliloti).			
OG	Plasmid pSymB (megaplasmid 2).			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
OC	Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.			
OX	NCBI_TaxID=382;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=1021;			
RC	MEDLINE=21396508; PubMed=11481431;			
RX	Finan T.M., Weidner S., Wong K., Buhmester J., Chain P., Chain P.,			
RA	Vorheiter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,			
RA	Golding B., Puehler A.,			
RA	RT "The complete sequence of the 1,583-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti."			
RA	Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).			
DR	AL613641; CAC49157..1; -.			
DR	PIR; E95936; E95936.			
DR	GO:0046821; C:extrachromosomal DNA: IEA.			
KW	Plasmid; Hypothetical protein; Complete proteome.			
SEQUENCE	256 AA; 28459 MW; 54B06434CECYC39 CRC64;			
Qy	3 WYASRGIRPYG 13			
Db	185 WHGTRGCRPYG 195			
RESULT 36				
Q8BUU8	PRELIMINARY;	PRT;	259 AA.	
ID	Q8BUU8;			
AC	Q8BUU8;			
DT	01-MR-2003 (TREMBLrel. 23, Created)			
DT	01-MR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Hypothetical pleckstrin homology.			
GN	C92005C14RIK.			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	NCBI_TaxID=10090;			

PRYOR M., Dutfoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
 RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Gordon R.G.,
 RT "The complete genome sequence of Mycobacterium bovis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8777-8782(2003).
 DR EMBL; BX218340; CAD9447.1; -.
 KW Complete Proteome;
 SQ SEQUENCE 276 AA; 30015 MW; 9107C098AEB5C904 CRC64;
 Query Match 50.0%; Score 41; DB 16; Length 276;
 Best Local Similarity 45.5%; Pred. No. 60;
 Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 WYASRGIRPVG 13
 Db 150 WFAAKEVKAVG 160

RESULT 40

Q8YNR3 PRELIMINARY; PRT; 546 AA.
 ID Q8YNR3
 AC Q8YNR3 ;
 DT 01-MAR-2002 (TREMBLrel: 20, Created)
 DT 01-MAR-2002 (TREMBLrel: 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel: 24, Last annotation update)
 DE Hypothetical protein Ali4499.
 GN ALL4499
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriuchi M., Itoh T., Matsukawa K., Kimura T.,
 RA Kohara M., Matsunoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpoo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213 (2001).
 DR EMBL; AP003596; BAB76198.1; -.
 DR PIR; AC2368; AC2368.
 DR InterPro; IPR001119; SLH.
 DR Pfam; PF00395; SLH; 1.
 DR PROSITE; PS01072; SLH.
 DR HYPOTHETICAL PROTEIN; Complete proteome.
 SQ SEQUENCE 546 AA; 58553 MW; 7A6A8E1961F72316 CRC64;
 Query Match 50.0%; Score 41; DB 16; Length 546;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 10; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
 Qy 2 AWY-ASRGIRPVGR 14
 Db 457 AWYVAAASGLIRDFFGR 471

Search completed: February 25, 2004, 06:43:51
 Job time : 40 secs